

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:09:03 ; Search time 14.16 Seconds  
(without alignments)  
1334.941 Million cell updates/sec

Title: US-09-715-962-2  
Perfect score: 4374  
Sequence: 1 MKRDMFSDGAVTFWIFLLCL.....LINSAAHATPAATLAIQTGE 840

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/PTCUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1158.5	26.5	859	3	US-09-183-253-2 Sequence 2, Appli
2	697.5	15.9	332	3	US-09-183-253-4 Sequence 4, Appli
3	359	8.2	908	4	US-08-855-146-2 Sequence 2, Appli
4	355.5	8.1	908	3	US-08-823-110-1 Sequence 1, Appli
5	355.5	8.1	908	3	US-08-604-298-1 Sequence 1, Appli
6	355	8.1	915	4	US-08-617-785-12 Sequence 12, Appli
7	355	8.1	922	4	US-08-617-785-14 Sequence 14, Appli
8	353	8.1	912	4	US-08-617-785-2 Sequence 2, Appli
9	353	8.1	915	1	US-08-453-862-2 Sequence 2, Appli
10	353	8.1	915	2	US-08-452-734A-2 Sequence 2, Appli
11	353	8.1	915	4	US-08-176-401B-2 Sequence 2, Appli
12	353	8.1	915	5	PCT-US94-14989-2 Sequence 2, Appli
13	349.5	8.0	912	5	PCT-US91-09422-19 Sequence 19, Appli
14	328	7.5	879	1	US-08-072-574-6 Sequence 6, Appli
15	328	7.5	879	1	US-08-486-270-6 Sequence 6, Appli
16	328	7.5	879	3	US-08-367-264-6 Sequence 6, Appli
17	327	7.5	872	3	US-08-337-797A-2 Sequence 2, Appli
18	327	7.5	872	3	US-09-258-523-2 Sequence 2, Appli
19	321.5	7.4	867	4	US-08-617-785-4 Sequence 4, Appli
20	313.5	7.2	877	2	US-08-407-875-2 Sequence 2, Appli
21	311.5	7.1	877	3	US-09-126-280-2 Sequence 2, Appli
22	302.5	6.9	1180	4	US-08-660-148-2 Sequence 2, Appli
23	297.5	6.8	1212	4	US-08-660-148-5 Sequence 5, Appli
24	283.5	6.5	1180	1	US-08-486-270-8 Sequence 8, Appli
25	283.5	6.5	1180	3	US-08-367-264-8 Sequence 8, Appli
26	282.5	6.5	1180	1	US-08-072-574-8 Sequence 8, Appli
27	280	6.4	1056	2	US-08-687-289A-8 Sequence 8, Appli

28	278.5	6.4	1212	1	US-08-486-270-10	Sequence 10, Appli
29	278.5	6.4	1212	3	US-08-367-264-10	Sequence 10, Appli
30	276.5	6.3	1212	1	US-08-072-574-10	Sequence 10, Appli
31	276	6.3	906	3	US-08-486-270-2	Sequence 2, Appli
32	276	6.3	906	3	US-08-367-264-2	Sequence 2, Appli
33	276	6.3	1194	4	US-08-538-526-1	Sequence 1, Appli
34	275.5	6.3	905	1	US-08-072-574-2	Sequence 2, Appli
35	273	6.2	1056	2	US-08-687-289A-7	Sequence 7, Appli
36	268	6.1	906	5	PCT-US91-09422-17	Sequence 17, Appli
37	268	6.1	1199	1	US-08-041-538-2	Sequence 2, Appli
38	268	6.1	1199	1	US-08-463-642-2	Sequence 2, Appli
39	268	6.1	1199	1	US-08-455-602-2	Sequence 2, Appli
40	268	6.1	1199	2	US-08-465-157-2	Sequence 2, Appli
41	268	6.1	1199	5	PCT-US91-09422-2	Sequence 2, Appli
42	265.5	6.1	877	1	US-08-486-270-12	Sequence 12, Appli
43	265.5	6.1	877	3	US-08-367-264-12	Sequence 12, Appli
44	263.5	6.0	877	1	US-08-072-574-12	Sequence 12, Appli
45	243	5.6	1058	2	US-08-687-289A-5	Sequence 5, Appli

## ALIGNMENTS

RESULT 1  
US-09-183-253-2  
; Sequence 2, Application US/09183253  
; Patent No. 6043054  
; GENERAL INFORMATION:  
; APPLICANT: VAWTER, LISA  
; APPLICANT: STAMMERS, MELANIE  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ratner & Prestia  
; STREET: P.O. Box 980  
; CITY: Valley Forge  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/183,253  
; FILING DATE: 30-OCT-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 9817907.0  
; FILING DATE: 17-AUG-1998  
; APPLICATION NUMBER: 60/075,306  
; FILING DATE: 20-FEB-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Prestia, Paul F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GP-70395  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0700  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 859 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-183-253-2

Query Match 26.5%; Score 1158.5; DB 3; Length 859;  
Best Local Similarity 31.8%; Pred. No. 8.5e-109;

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Matches 268; Conservative 158; Mismatches 296; Indels 121; Gaps 19;
QY 18 ICLIASPHLQGVAGRP-----DELHIGGIPI-----AGKGWQGGQACMPATRLALDDV 68
Db 16 LLLPLAPAGWARGARPPSPPLSLINGLPLTKREVAKSI--GRGVLPVELAIEQI 73
QY 69 NKQPNLLPGFKLLHSNDSECEPGLGASVYNNLLYKNPKOKMLLAG-CSTVCTTVAEAK 127
Db 74 RNESLLRPYF-LDLRYDTECDNAKGLKAFYDAIKYGNHLMVFGGVCPSVTIIAESLQ 132
QY 128 MNLLVLCVAGSSPALSDDRKPFTLRTPHSATVHNPTRIKLMKFGWSVAILOQAEV 187
Db 133 GNNVLQSFAPATPVADKKKPYFRTVPSDNVAVNPAILKLLKHQWKVGTLTQDVQR 192
QY 188 FISTVEDLENRMEAGVEIVTRQSFLSDPTDAVRNLRQDARIIVGLFYVVAARRVLCME 247
Db 193 FSEVRNDLTGLVGEDIEISDFESFNDPCTSVKLLKNDVRIILGQFDQDMAKVC-- 250
QY 248 YKQQLYGRAHVFFIHWEDNWEVNLKABGICTCTVEQRIAAEGHLLTTEALMWNQNT 307
Db 251 -----CTPQQ-----YREYNN 262
QY 308 TISGMTAEFRHRLNQAITEGVDINHRYPEGYQAPLAYDAVWSVALAFNKTMERL-- 365
Db 263 KRSGVPSKF-----HGY-----AYDGIWIAKTLQRAMETLHA 296
QY 366 TTGKSLRDFTYTDKEIADEIYAAMNSTQFLGSGVVAFFSSQGDRIALTQIEQMIDGKYE 425
Db 297 SSRHQRIQDFNTDHTLGRILLNAMNETNFFGVTVGVVFRN-GERMGTIKFTQFQDSREV 355
QY 426 KLGYDTQLDNLISWLN-TEQWIGGKVPQDRTIVTHVLRVSLPLFVCMCTISSCGIFVAF 484
Db 356 KYGEYNAVADTLEIINDTIRFQSGSEPPKDKTIILEQLRKISLPLSYLSALTILGIMTAS 415
QY 485 ALIIEINWKRHRVIOSSHVPVNTIMLFGVILICLSVILLGIDGRFVSPPEYPKICOARA 544
Db 416 AFLFNKRNOKLIKMSPPYNNLLIILGMLSYASIFLFGDGSFVSEKTFETLCVTRT 475
QY 545 WLLSGFTLAYGAMFSKVRVHRTTKAKTDPKKKKVPKMLYTMVSGLLSIDVILLSWQ 604
Db 476 WILTVGYTTAFGAMFAKTRVHAIFKNVKM-KKKIKDKQLLVIVGMLLIDILICILCWQ 534
QY 605 IFDPLQRYLETPLLE-DPVSTTDDIKIRPELEHCESSQNRSMWGLVYGFGLILVFGFL 663
Db 535 AVDPLRLRTVEKYSMEPDAGR--DISIRPLEHCENTHMTIWLGIYVAYKGLLMFGCFL 592
QY 664 AYETRSIKVQINDSRVGVMSIYNNVVLCLITAPVGVVIASQODASFAFVALAVIFCCFL 723
Db 593 AWETNRVSPALNDSKYIGSVYNNVIMCIIGAASFLTRDQPNVQFCIVALVIFGCTI 652
QY 724 SMLLIFVPKVIEWIRHP-----KDAESKYNPD-SATSKEDDEERYOKLVT 768
Db 653 TILCFVPKLIYLRTPDAATQNRREFQTNQKKEDSKTSTSVTSVNOASTSRLEGQSE 712
QY 769 NEQLQRLITQKEKIRVLQRRLVERGDAGT-----ELNGATGVASAAVATTSQAS 820
Db 713 NHRLRMKITELDKDLEEVMTQLDTEP-KTYTIKQNHQYELNIDILNIGNFTESDGGKAI 771
QY 821 LIN 823
Db 772 LKN 774
RESULT 2
US-09-183-253-4
; Sequence 4, Application US/09183253
; Patent No. 6043054
; GENERAL INFORMATION:
; APPLICANT: VAWTER, LISA
; APPLICANT: STAMMERS, MELANIE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/183,253
; FILING DATE: 30-OCT-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9817907.0
; FILING DATE: 17-AUG-1998
; APPLICATION NUMBER: 60/075,306
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70395
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-183-253-4
Query Match 15.9%; Score 697.5; DB 3; Length 332;
Best Local Similarity 41.4%; Pred. No. 1.7e-62;
Matches 135; Conservative 74; Mismatches 110; Indels 7; Gaps 6;
QY 372 LRDTYTDKEIADRIYAAMNSTQFLGSGVVAFFSSQGDRIALTQIEQMIDGKYELGYD 431
Db 2 IQDFNYTDHTLGRILLNAMNETNFFGVTVGVVFRN-GERMGTIKFTQFQDSREVKVGYN 60
QY 432 TQLDNLISWLN-TEQWIGGKVPQDRTIVTHVLRVSLPLFVCMCTISSCGIFVAFALIIFN 490
Db 61 AVADTLEINDTIRFQSGSEPPKDKTIILEQLRKISLPLSYLSALTILGIMTASAFLEFN 120
QY 491 IWNKRRVIOSSHVPVNTIMLFGVILICLSVILLGIDGRFVSPPEYPKICOARALLSTG 550
Db 121 IKNRQKLIKMSPPYNNLLIILGMLSYASIFLFGDGSFVSEKTFETLCVTRTWILVVG 180
QY 551 FTLAYGAMFSKVRVHRTTKAKTDPKKKKVPKMLYTMVSGLLSIDVILLSWQIFDPLQ 610
Db 181 YTTAFGAMFAKTRVHAIFKNVKM-KKKIKDKQLLVIVGMLLIDILICILCWQAVDPLR 239
QY 611 RYLETFFPLE-DPVSTTDDIKIRPELEHCESSQNRSMWGLVYGFGLILVFGFLAYETRS 669
Db 240 RTVEKYSMEPDAGR--DISIRPLEHCENTHMTIWLGIYVAYKGLLMFGCFLAWETR 297
QY 670 IKVQINDSRVGVMSIYNNV-VVLCLI 694
Db 298 VSPALNDSKYIGSVYNNVNGIISCR 323
RESULT 3
US-08-855-146-2
; Sequence 2, Application US/08855146
; Patent No. 6221609
; GENERAL INFORMATION:
; APPLICANT: Belagaje, Rama M.
```

APPLICANT: Wu, Su  
TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center/Patent Department  
CITY: Indianapolis  
STATE: IN  
COUNTRY: USA  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/855,146  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/021,243  
FILING DATE: 07-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Webster, Thomas D.  
REGISTRATION NUMBER: 39,872  
REFERENCE/DOCKET NUMBER: X-10836  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-6334  
TELEFAX: (317) 276-2764  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 908 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-855-146-2

Query Match 8.28; Score 359; DB 4; Length 908;

Best Local Similarity 21.18; Pred. No. 4e-27; Mismatches 378; Indels 232; Gaps 44;

13 FWIFLLCLIASPHLQGGVAG-RPD-ELHIGGIFPIAGKGGWGGQAC-----MP 59  
22 YWI--LTMQTHSQEYAHSTRVDGDIILGGLFPVHAG--ERGVPCGELKKEGIHRL 77  
60 ATRALDDVNKOPNLPFKL---IL-----HSNDSCEPGL 93  
78 AMLYAIQIDKDPDLSNITLGVRLDTCSDTYALEQSLTFVQALIEKDSADKVCANGD 137  
94 GASVYNNLYNKPOL--MLLAGSTVCTTYAEAAKMNVLVLCYGASSPALSDEKRPPT 151  
138 PP-----IFTKPKISGVIGAAASSVIMANILRLFKIPQISYASTAPELSDNTRYDF 191  
152 LFRTPSPVHNPRTRIKLMKFGWSRAVILQAAEVEFTSTVEDLENRCWE-AGVEIVTRO 210  
192 FSRVVPDSYQAQAMVDIVLTALGNWYVSTLASSENGYSGSVEAFQISREIGGVCIASQ 251  
211 SFLSDPTDA-----VRNLRQDARIIVGLFYVVAARVLCMEYKQQLYGRAHVWFFIGW 264  
252 KIPREPRGEPIKIRLETPNARAVIMFANEDDIRILEAAKLNOSGH---FLWIG- 307  
265 YEDNW-----YEVNLKAEITCTVEQMRTAAEG---HLTEALMNQNONOTTISGMTA 314  
308 -SDSWGSKIAPVQOEETAEAG-AVTILPKRASIDGDFRFSRSTLANNRRV-----WFA 360  
315 EEFHRLNQAALIERGYDINHDPYEGY-----QEAFLAY--DAVWSVALAFNKT 362  
361 EFWEENFGCKLSGSHGRKRNHSHKCTGLERIARDSSYQEGKVQFVIDAVYSMAYALHNMH 420  
363 ERLTGTGKSL--RDFVTYDKEIADEIYVAMNSTOFLGVSGV-VAFSSOGDRALFOIEQ- 418

Db 421 KDLCPGYIGLCPRMSTIDGKELLYIRA-----VNFNGSAGTPTVTFNENGADPGRYDIFY 476  
QY 419 MIDGK---YEKLGYYDTQL-----DNLSQLNTEQWIGKVPQDRTIVTHVLTYSLP--- 467  
Db 477 QITNKSTEYKVIQHTWNLQHLKVEDMOWAHREH-----THPASVCSLPCKPG 523  
QY 468 -----LFVCMCTI-----SSC----- 478  
Db 524 ERKKTGKVPCCWHCEGCEGYNYQVDELSCELCPDQRPNNRGTGCOLIPIIKLEWHSPW 583  
QY 479 ---GIFVA-----FALLIENIWNKHRRVIOSSHVPVCNTIMLFGVILICLISVILLGID 527  
Db 584 AVVPFVAILGIATTFVIIVTFVRYN-DTPIVRASGRELSYVLLTGIFCYSITFLM--- 639  
QY 528 GRVSPDEEYKICQARAWLLSTGFTLAYGAMFKWVRHRTTKAK---TDPKKKVEPWK 584  
Db 640 --IAAPDTI--ICSFRVFLGLCMFCPSYAALLTKTNRIHRIFEQKKSVTAP-KFISPAS 694  
QY 585 LYTMVSGLLSIDLVLSWQIFDPLQRYLETFFLEDPVSTDDIKIRPELEHCEQSQRNM 644  
Db 695 QLVITFSLISVQLLGVFWFVDPPIIID-----YGEQRTLDPEKARGVLK-CDISDLSL 749  
QY 645 WLGLVYGFKGLIILVFLGLFAYETRSIKVKQINDSRVYVGMISYVNVVLCILITAPVGMVIA 704  
Db 750 ICSL--GYSILLMVTCTVYANKTRGV-ETFEAKPIGFTMYTCIIWLAFIPIFFGTQA 806  
QY 705 QODASE--AFVALAVIFCCFLSMILLFVPKVIETVRHPKDKAESKYNPDALSKEDEER 761  
Db 807 SAEKMYIOTTLLVSVMSLSASVSLGMLYMPKVIIIFHPQNVQKR-----KRS 855  
QY 762 YQKLVTENEQRLITQKEEKIRVLRQRLVERGDATGATGATGATGATGATGATGATGATGAT 821  
Db 856 EKAVVTAATMQSKLIQKGNDR-----PNGEVK-SEL-----CESLETNTSSTKTTY 900  
QY 822 INSSAHA 828  
Db 901 ISYNSHS 907

RESULT 4

US-08-823-110-1

; Sequence 1, Application US/08823110  
; Patent No. 6077675

; GENERAL INFORMATION:

; APPLICANT: Stormann, Thomas M.

; APPLICANT: Simin, Rachel T.

; APPLICANT: Hammerland, Lance G.

; APPLICANT: Fuller, Forrest H.

; TITLE OF INVENTION: NOVEL HUMAN METABOTROPIC

; TITLE OF INVENTION: GLUTAMATE RECEPTOR

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: FastSeq for Windows 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/823,110

; FILING DATE: March 24, 1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/604,298

; FILING DATE: February 21, 1996

; ATTORNEY/AGENT INFORMATION:

```

; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/259
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 908 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-08-8223-110-1

Query Match      8.1%; Score 355.5; DB 3; Length 908;
Best Local Similarity 21.1%; Pred. No. 9.1e-27;
Matches 194; Conservative 147; Mismatches 363; Indels 217; Gaps

QY 13 FWIFLLCLIASPHLQGGVAG-RPD-ELHIGGIFPIIAGKGGWGQOAC-----MP 59
   || || || || || || || || || || || || || || || || || || ||
Db 22 YWI-LTMQTHSQEYAHSIRVDGDIILGGLFPVHAKG--ERGVPGELKKEKGHRL 77

QY 60 ATRLALDDVKNQNLPLPGFKL---IL-----HSNDSECEPGL 93
   | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 78 AMLYAIDQINKDPDLSNITPLGVRIIDTCSRDTYALEQSLTFVQALIERKADSDVRCAMD 137

QY 94 GASVMYLLNKKPKQL--MLLAGCSWTCVTVAEAAKWNLIIVLCYGASSPALSDKRKPT 151
   || || || || || || || || || || || || || || || || || || ||
Db 138 PP-----IFTKPDKISGVIGAASSVIMVANILRLRFIPQISYASTAPELSDNTRDYF 191

QY 152 LFRTHPSATVHNPTRIKMKKFGWSRVAILQAAEEYFISTVEDLENRCME-AGVEIVTRQ 210
   || || || || || || || || || || || || || || || || || || ||
Db 192 FSRVVPDSYAQAAMVDIVTALGMVNVYSTLASBNGYSGSVEAFTQISREIGGVCTIAQSQ 251

QY 211 SFLSDPTDA-----VNLRRQDARIIVGLFYVAARRVLCEMYKOOLYGRAHVWFFIGW 264
   || || || || || || || || || || || || || || || || || || ||
Db 252 KIPREPRGGEFKIIRLLETPPNARAVIMFANEDDIRRIEAAKLNQSGH---FLWIG- 307

QY 265 YEDNW-----YEVNLKAEGICTVTEOMKRIAAEG---HLTTEALMWNONNQTTSIGMTA 314
   || || || || || || || || || || || || || || || || || || ||
Db 308 -SDSWGSKIAPVQQOEIAEG-AVTILPKRASIDGDFRFSRSTLANNRNV-----WFA 360

QY 315 EEFRRLNQALIEEGYDINHRYPEGY-----QEAPLAY--DAYMSVALAFNKTIM 362
   | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 361 EFWEENFGCKLHGSHGRKNSHIKKCTGLERTARDSSYEQEGKVQFIDAVYSMAALHNHM 420

QY 363 ERLTGTGKSL--RDFYTDKEIADELYAAMNSTQFLGVSGV-VAFSSQGRALTALQIEQ- 418
   | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 421 KDLCPGYIGLCPRMSTIDGKELGYIRA----VNFNGSAGTPVTFNENGDAFGRVDIFOY 476

QY 419 MIDGK---YEKLAGYDPTQL----DNLSWLNTEQWIGKVPQDRTIIVTHVLRVTSLP---- 467
   || || || || || || || || || || || || || || || || || || ||
Db 477 QITNKSTEYKVIQHTNQLHLKVEDMQWAHREH-----THPASVCSLPCPKG 523

QY 468 -----LFCVCMCTI-----SSC----- 478
   | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 524 ERKKTIVGVPCCWHCECEGYNTQVDELSCELPQLQRPNNMTGCOLPIIKLEWHSWP 583

QY 479 --GIFA-----FALLIENLWKKHRRVIOSSHPVCNTIMLFGVVIICLSVILGLID 527
   || || || || || || || || || || || || || || || || || || ||
Db 584 AVVPFVAILGIATTFVITVFVRYN-DTPIVRASGRESLYLLTGIFLCYSITFLM--- 639

QY 528 GRFYSPEYPRKICQARAWLLSTGFTLAYGAMFVKVRVHRFTTKAK---TDPRKKKPEPWK 584
   || || || || || || || || || || || || || || || || || || ||
Db 640 --IAAPDTI--ICSFERRVFLGLMCFSYAALLKTNRIHRIEFGQKKSVTAP-KFISPAS 694

QY 585 LYTMVSGLLSIDLIVLLSQIFDPLQRYLETFPLEDPVSTDDIKTRPELHCECORSNM 644
   | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 695 QLVATFSLISVQLLGVFVFWFVDPPIIID----YGEQRTLDPEKARGVLK-CDTSDLSL 749

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Qy   645 WGLGVYGEKGLLVFGLFLAYETRSIKVKQINDSRYVGSIMYNVVLCCLITAPVGWAVIAS 704
      | : || : || : || : || : || : || : || : || : || : || : || : || :
Db   750 ICSL--GYSILLMTCTVYAIAKTRGVP-ETFNEAKPIGFMTYTTCIIWLAFIPFFGTQA 806
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy   705 QQDASE---AFVALAVIFCCFLSMLLIFVPKVIWIRHPDKAESKYNPDALSISKEDEER 761
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   807 SAENMYIQTTTLTVTMSLSASVSUGMLMPKVYIIFIHPSNVOKR-----KRS 855
      : : || : || : || : || : || : || : || : || : || : || : || :
Db   856 FKAVVTAATMQSKLIQKNDR 876
      : : || : || : || : || : || : || : || : || : || : || : || :

RESULT          5
US-08-604-298-1
; Sequence 1, Application US/08604298
; Patent No. 6084084
; GENERAL INFORMATION:
; APPLICANT: Stormann, Thomas M.
; APPLICANT: Simin, Rachel T.
; APPLICANT: Hammerland, Lance G.
; APPLICANT: Fuller, Forrest H.
; TITLE OF INVENTION: NOVEL HUMAN METABOTROPIC
; TITLE OF INVENTION: GLUTAMATE RECEPTOR
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/604,298
; FILING DATE: February 21, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 908 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-08-604-298-1

Query Match           8.1%; Score 355.5; DB 3; Length 908;
Best Local Similarity 21.1%; Pred. No. 9.le-27;
Matches 194; Conservative 147; Mismatches 363; Indels 217; Gaps

Qy   13 EFWILFLCLIASPHLGGVAG-RPD-ELHIGGFPTAGKGHGQGOAC-----MP 59
      :||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :
Db   22 YWI---LTWMQTHSEYAHNRVDGDITLGLFPVHAKG---ERGVPCELKKKGIIHRLE 77
      :||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :
Qy   60 ATRLALDVNKQPNIPLPGFKL---IL-----HSNDSECPGL 93

```

```
Db 78 AMLYDAIDQNDPDLNITLGVRLDTCSDRTYALRQSLTFVQALIERKXSDVRCANGD 137
Qy 94 GASVYNNLYNKPQKL--MLLAGCSTVCTTVAEAAKMNLIIVLCYGASSPALSDRRFPT 151
Db 138 PP-----IFPKPKISGVGAASSVIMVANIILRPKIPQISVASTAPELSDNTRYDF 191
Qy 152 LFRTHPSATVNPTRIKMLKFGNSRVAILOQAEEVFISTVDLENRCME-AGVEIVTRQ 210
Db 192 FSRVVPDPSYQAQMDIVTALGVNVSTLASEGVNGSEGVAFQISREIGGVCIQAQSQ 251
Qy 211 SFLSDPTDA-----VRNLRQDARIIVGLFVVAARRVILCEMYKQOLYGRAHVFFIGW 264
Db 252 KIPREPRGEFEKIIRLLETPNRAVIMFANEDDIRILEAAKLNQSGH---FLWIG- 307
Qy 265 YEDNW-----YEVNKAEGITCIVEQMRTAAEG---HLTTEALMNNQNTTISGMTA 314
Db 308 -SDRWGSKIAPYQOEIAG-AVTILPKRASIDGDFRFRSRTLANNRRV-----WFA 360
Qy 315 EEFRRHLNQAILEGYDINHRYPEGY-----QEAPLAY--DAVMSVALAFNKT 362
Db 361 EFWEENFCGLGSHGKRNHSHKCTGLERIARDSSVEQEGKVQFVIDAVYSNAYALHNNH 420
Qy 363 ERLTTGKKSLL--RQFTYTDKEIADBIYAAAMNSTQFLGSGV-VAFSSQGDRIALTOIEQ- 418
Db 421 KDLCPGYIGLCPRMSTIDGKELLYIRA---VNFNGSAGTPTVTNFENGADPCRYDIFQY 476
Qy 419 MIDCK---YEKLYGYDTOL---DNLSWLNTEQWIGGVQPQDRTIVTVLRTVSLP--- 467
Db 477 QITNKTSTEYKIVIGHWTNOLHLKVEDMQWAHREH-----THPASVCSLPCRP 523
Qy 468 -----LFVCMCTI---SSC----- 478
Db 524 ERKKTIVGVPCWCHCEGEGYNOVDELSCELCPLDQRPNNRTGCQLPIIKLEHSPW 583
Qy 479 ---GIFVA-----FALIIFNIWKNHRRVIQSSHPVCNTIMLFGVILCLISVILLGD 527
Db 584 AVVPFVAILGIIATTFIVITFVRYN-DTPIVRASGRELSYVLLGIFLCYSITFLM--- 639
Qy 528 GRFVSPPEYKICQARAWLLSTGFLAYCAMFSKVVWRHRTTAK---TDPKKKVEPK 584
Db 640 --IAAPDI--ICSFRRVFLGLGMCFSYAALLTKTNHRIFEQKKSVTAP-KFISPAS 694
Qy 585 LYTMVSGLLSIDLVLISQWIFDPLQRYLETFFPLEDPDPTSTDIIKIRPELEHCESNRM 644
Db 695 QLVITFSLISVOLGCVFWFVDDPHIID---YGEQRTLDPEARGVLK-CDISDLSL 749
Qy 645 WLGLVYFGKILVGLFLAYETRSIKYKQINDSRVGMGIYNNVVVLCLITAPVGMVIAS 704
Db 750 ICSSL--GYSILLMTVCTVYAIKTRGV-ETFEAKPIGFTMYTTCIILWLAFTPIFFGTAQ 806
Qy 705 QODASF---AFVALAVIFCCFLSMILLIIVPKVIEVIRIPKKAESKYNPDISAIXEDEER 761
Db 807 SAEKMYIQTTLTVTSMISLASVSLGMLYMPKYIIIFHPEQNVQKR-----KRS 855
Qy 762 YOKLVTENEQRLQRLTOKEEK 782
Db 856 FKAVVTAATMOSKLIQKGNDR 876
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## RESULT 6

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US-08-617-785-12
; Sequence 12, Application US/08617785E
; Patent No. 6228610
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttnier, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
; FILE REFERENCE: 4-19679/A/PCT
```

```
; CURRENT APPLICATION NUMBER: US/08/617,785E
; CURRENT FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: PCT/EP94/02991
; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-617-785-12
```

```
Query Match 8.1%; Score 355; DB 4; Length 915;
Best Local Similarity 21.5%; Pred. No. 1e-26;
Matches 209; Conservative 153; Mismatches 319; Indels 292; Gaps 50;
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Qy 17 LLCLIA-----SPH---LOGGVAGRDELDHIGGIFPIAGKGGWQGGQAC----- 57
Db 24 LICALAAAARGQEMYAPHSIRIEGDT-----LGLFPVHAKG--PSGVPCGDIKREN 74
Qy 58 ---MPATRLALDDVANKQPNLLPGFKL---IL-----HNSDS 87
Db 75 GIHRLLEAMLYALDQINSDPNLLPNVILGARILDTCSRDYALRQSLTFVQALIQKDTSDV 134
Qy 88 ECEPGLGASVYNNLYNKPQKMLLAGC---STVCTTVAEAAKMNLIIVLCYGASSPALSD 145
Db 135 RCTNGEPP-----VFVKPEKVVGVIGASGSSVIMVANIILRLFIQIPQISVASTAPELSD 188
Qy 146 RRFPFLFRTHPSATVNPTRIKMLKFGHSRVAILOQAEEVFISTVDLENRCMEAGVE 205
Db 189 DRYDFFSRVVPPDSFQAQAMVDIVKALGNW-----XVSTLAS-EGSYGEGKVE 236
Qy 206 IVTRQSFSDPTDAVNLR---RQDA-----RIIVGLFVYVAARRVLC---EMVKKOOL 252
Db 237 SFTQISKEAGGLCIAOSVRIPQERKORTIDFRIIKQLDTPNSRAVIFANDEDIKQIL 296
Qy 253 YG--RA-HVWFFTGWYEDNW-----YEVNKAEGITCIVEQMRTAAEG---HLTTEAL 299
Db 297 AAAKRAQVGHFLWVGSDSGSKINPLHQHEDIAEG-AITIQPKRATVEGDAYFTSRTL 355
Qy 300 -----MW-----NONQOTTISGTAEEF-RHRLNQAILEGYDINHRYPEGVQEAP 345
Db 356 ENNRNVWFAEYWEENFNCKLTISGSKEDTRKCTGQERI--GKDSNYEQ--EG--KVQ 409
Qy 346 LAYDAVMSVALAFNKTMERLT-----GKSLRDTFTYTDKEIADFIYAAMNS 392
Db 410 FVIDAYAMAHUHHNKNKDLCAHYRGVCPMEQAGGKKLLK-----YIRN 454
Qy 393 TQFLGVSGV-VAFSSQGDRIALTOIEQMDIGYKELGYDTQLDNLW-----L 440
Db 455 VNFNGSAGTPVMEKNKD-----APGRYDIFQYQTTNTSNPCYRLIGQWDELQQL 504
Qy 441 NTE--QWIGG--KVP----- 451
Db 505 NIEDMQWKGVRIPASVCTLPCKPGQRKKTQGTCCWTCPCDGYQYQFDEWTCQHCP 564
Qy 452 -----QDRTIVT---HVLRTVSLPLFVCMCTISSCGIFVAFALIININKHR 496
Db 565 YDQRPNENRTGQODIPIIKLEHSPWAV-IPVFLAMLGIITAT-IFVMTATFIRYN---DT 618
Qy 497 RVIOSSHPCVNTIMLFGVILCLISVILLGIDGRFVSPPEYKICQARAWLLSTGFTLAYG 556
Db 619 PIVRASGRELSVLLTGIFLCYIITFLM-----IAKPD--VAVCSFRRVFLGLGMCISYA 671
Qy 557 AMFSKVVWRHRTTAK---TDPKKKVPWKLYTMVSGLLSIDLVILLSSQIDFPLQRYL 613
Db 672 ALLTKNRIYRIFEQKKSVTAP-RLISPTISQLAITSSLSVQLLGVFIWFGVDPNNIIL 730
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ORGANISM: Homo sapiens  
US-08-617-785-2

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Query Match      8.1%; Score 353; DB 4; Length 912;
Best Local Similarity 18.5%; Pred. No. 1.6e-26;
Matches 169; Conservative 179; Mismatches 371; Indels 196; Gaps 38;

QY 13 FWIFL-LCLIAS-----PHLGGVAGRP-----DELHIGGIFPIAGKGWGGQAC 57
DB 10 WVARPLCLLLSLYGPWMPSSLGKPKGPHMNSIRIDGDIITGLGFPVHGRG--SBGKPC 67
QY 58 -----MPATRLALDDVNKQNLPLPGFKL-----IL 82
DB 68 GELKKEGHIHLEAMLFALDRINDDPLNITLITGALDTCSDTHALEQSITFVQALI 127
QY 83 HNSDSECEPGLGASWYNLLYNKPKMLLAGC--STVCTTVAEAAKWNLLIVLCYGASS 140
DB 128 EKDGTVEVCGSGGPP-----IITKPERVGVIGAGSSSVSIMVANILRLFKIPQISYASTA 183
QY 141 PALSDRKRPFTLFRTHPSATVHNPTRIKMKFGWSRAIL-----QOAEVEFISTVE 193
DB 184 PDLSDNSRYDFSRVVPDSTYQAOAWDIVRALKNYVSTVASEGSGYEGVEAFIOKSR 243
QY 194 DLENRCMEAGVEIVTQSFSLDPTDAVRN--LRRODARIIVGLFYVVAARRVLCVEMYKQOL 252
DB 244 EDGGVCIQAQSVKI--PREPKAGEFDKIIIRLLETSNARAVILFANEDDIRVLEAARRANQ 302
QY 253 YGRAHVWFIFIGWYEDNW-----YEVNLKAEG--ITCIVTEQMRIAAEGLHITTEALMNQ 304
DB 303 TGH---FFWVG--SDSWGSKTAPVLHLEEAAGAVTILPKRMSVRGDFRYFSRTLDNRR 357
QY 305 NOTTISGMTAEFRHLNOALIEEYDI---NHDRYPE--GYOE---APLAYDAWWSVA 355
DB 358 RNIFAEFEWENFCHLKHALKSHVKKCTNRNREGODSAYEQEGKVQFVIDAVIANG 417
QY 356 LAFNKTMERLTGKSLRDFTYTKEIADEIYAAMNSTQFGLVSG--VVAFFSQGD---RI 411
DB 418 HALHAMHRDLCPGRVGL--CPRMPDVGDTOLLKYIRNVNFSGIAGNPVTFNENGDPGRY 475
QY 412 ALTOIEQIMD--GKYEKLG----YDTQDLNLSWLNTEQWIGKV-----PQDR----- 454
DB 476 DIYOYQLRNDSEAYKVIKGSWTDHLHLRIERMHWPGSGQOLPRISICSLPCQPGERKKTVK 535
QY 455 -----TIVTHVLRT-----VSLPLFVC 471
DB 536 MPCWCWHCEPCTGYOYQVDYRTCKTCTPYDMRPTENTGCRPIPIIKLEWSPWAVLPLFLA 595
QY 472 MCTISSCGIFVAFALIIFNIWKNHRRVIOSSHPVCNTIMLFGVILICISVILLGIDGRV 531
DB 596 VVGIAAT--LFVVIIFVRN-----DTPPIVKAAGRELSYVLLAGIFLCYATTFM-----IA 645
QY 532 SPEYYPKICQARAWLLSGFTLAYGAMFSKVMVRHRETTKAK--TDPKKKVEPKWLYTMV 589
DB 646 EPD--LGRCSLRRIFLGLGMSISYAALLTKNRIYRIEIQGKRSVSAPRIFISPOLAIT 703
QY 590 SGLISIDVILLWQIDPDLQRYLETFFLEDVSTDDIKRPELEHESQNSWMLGLV 649
DB 704 FSLISLQLGLICVWFVDDPSHVVDD---FQD--QRTLDPRFARGVLKCDI--SDLSLCL 756
QY 650 YGFGLILVFLFLAYETPRSKVQINDSRVGVMSIYNVVLCLITAPVGMVIAQQOAS 709
DB 757 LGYENMLAVTCTVVAIKRGVP--EWFNEAKPIGFTWYTTCIVWLAFIGPI--FFGTSQAS 813
QY 710 FAFV-----ALAVIFCCFLMLLIFVPKVEIVIRPKDKAESKYNPDNSAISKEDEERTOK 764
DB 814 KLYIQTTTLTVSVLSASVSLGMLYMPKVIILFHPQNVPR-----KRSILK 861
QY 765 LVTENEQLORLITOK 779
DB 862 AVVTAATMSNKTOK 876
```

```
RESULT 9
US-08-453-862-2
: Sequence 2, Application US/08453862
: Patent No. 5738999
: GENERAL INFORMATION:
: APPLICANT: Segerson, Thomas P.
: APPLICANT: Kinzie, J. Mark
: APPLICANT: Mulvihill, Eileen R.
: APPLICANT: Saugstad, Julie A.
: APPLICANT: Westbrook, Gary L.
: TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Crew LLP
: STREET: Two Embarcadero Center, 8th Floor
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/453,862
: FILING DATE: 30-MAY-1995
: CLASSIFICATION: 436
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/176,401
: FILING DATE: 30-DEC-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Parmelee, Steven W.
: REGISTRATION NUMBER: 31,990
: REFERENCE/DOCKET NUMBER: 13952-18-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-467-9600
: TELEFAX: 415-576-0300
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 915 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-453-862-2
```

Query Match 8.1%; Score 353; DB 1; Length 915;  
Best Local Similarity 21.2%; Pred. No. 1.7e-26;  
Matches 206; Conservative 156; Mismatches 320; Indels 290; Gaps 50;

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QY 17 LCLLIA-----SPH---LOGGVAGRPDELHIGGIFPIAGKGWGGQAC----- 57
DB 24 LLCVLAARAAQGMVAPHISIRIEGDTV-----LGGLFPVHAKG--PSGVPCGDIKREN 74
QY 58 ----MPATRLALDDVNKQNLPLPGFKL---IL-----HSNDS 87
DB 75 GHIRLEAMLYALDQINSNDPLNPLNVTLGARILDTCSRDTYALQSLTFVQALIQKDTSDV 134
QY 88 ECEPGLGASWYNLLYNKPKMLLAGC--STVCTTVAEAAKWNLLIVLCYGASSPALSD 145
DB 135 RTNGEPPP-----VFKPEKVVGVIGAGSSSVSIMVANILRLFKIPQISYASTAPELSD 188
QY 146 KRKFPTLFRTHPSATVHNPTRIKMKFGWSRAILQOAEVEFISTVEDLENRCMEAGVE 205
DB 189 DRRYDFSRVVPDPSFOAQAWDIVKALGNW-----YVSTLAS--EGSYGEKQVE 236
QY 206 IVTRQSFSLDPTDAVRNLR-----RQDA-----RIIVGLFVVAARRVLC-----EMTKQOL 252
DB 237 SFTQISKEAGGLCIAQSVRIQPKRQKRTIDFDRIIKQLLDTPNSRAVWIFANEDIKQIL 296
QY 253 YG--RA--HYWFFIGWYEDNW-----YEVNLKAEGITCTVEQMRIAAEG---HLTEAL 299
```

Db 297 AAARADQVGHFLWVSDSGSKINPLHQHEDIAEG-AITIQKRAVTEGFDAYFTSRTL 355  
QY 300 -----MW-----NONNOTTISGMTAEF-RHRLNQALIEEGYDINHDPYEGYQAP 345  
Db 356 ENNRNVWFAEYWEENFNCKLTISGSKKEDTDRKCTGQERI--GKDSNYEQ--EG--KVQ 409  
QY 346 LAYDAVWSVALAFNKTMERLTT-----GKSLRDTFTYDKEIADEIYAAMNS 392  
Db 410 FVIDAVYAMAHALHMHNMKDCADYRGVCPMEQAGGKLLKYIRHVN----- 456  
QY 393 TQFLGVSGV-VAFSSQDRIALTQIEQMDGKYKGLGYDTQDNLWS-----L 440  
Db 457 --FNGSAGTPVFNKNGD-----APGRYDIFQYQTNTNPGYRLIGQWTDLQL 504  
QY 441 NTE--QWIGG--KVQ-----DRTIVTH-- 459  
Db 505 NIEDMQMGKGVREIPSSVCTLPCKPQRRKTKGTGCCWTCPCDGYQYQFDEMTQCHP 564  
QY 460 -----VLRT-----VSLPLFCMCTISSCGIFVAFALIFNINWKKRR 497  
Db 565 YDQRPENRTGCONIPDIKLEWHSWAVIPVFLAMLGIIAT-IFVMTATFIRN-----DTP 619  
QY 498 VIQSHRPVNTIMLFGVILICLSVILLGIDGRFVSPEEYPKICQARAWLLSTGFTLAYGA 557  
Db 620 IVRASGRELSSVLLTGIFLCYIITFLM-----IAKPD--VAVCSFRVFLGLCMCISYAA 672  
QY 558 MFSKVMVRHFTTAK---TDPKKVEPWKLYPMVSGLLSIDLVLLSMQIFDPLQRYLE 614  
Db 673 LLTKTNRIRYRIFEQGKKSVTAP-RLISPTSQLAITSSLSVQLLVFVFGVDPNPIID 731  
QY 615 TFPLEDPVSTDDIKIRPLEHCESSORNSMWGLVYGFGLIILVFLAYETRSIKVKQ 674  
Db 732 ---YDEHTMPEQARGVLK-CDITDLQIICSL--GYSILLMVTCTVVAIKTRGVP-EN 783  
QY 675 INDSRVGMSIYNNVVLICITAPVGMVIAISOQDASFAV-----ALAVIFCCFLSMILLIF 729  
Db 784 FNEARPIGTMTTTCIVWLAFPI--FFGTAQSAEKLYITTTLTISMNLSASVALGMLY 841  
QY 730 VPKVIEVIRHPDKAESKNPDISAISKEDEERYQKLVTEQQLRLITQKEEKIRVLQR 789  
Db 842 MPKVYIIIFHPELNVQKR-----KRSFKAVVTAATMSRSLSHKPSDR----- 883  
QY 790 LVERGDAGKTEL 801  
Db 884 --PNGEAK-TEL 892

## RESULT 10

US-08-452-734A-2  
; Sequence 2, Application US/08452734A  
; Patent No. 5831047  
; GENERAL INFORMATION:  
; APPLICANT: Segerson, Thomas P.  
; APPLICANT: Kinzie, J. Mark  
; APPLICANT: Mulvihill, Eileen R.  
; APPLICANT: Saugstad, Julie A.  
; APPLICANT: Westbrook, Gary L.  
; TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08452,734A

FILING DATE: 30-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/176,401  
FILING DATE: 30-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-18-1  
TELEPHONE: 206-467-9600  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 915 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-452-734A-2

Query Match 8.1%, Score 353; DB 2; Length 915;  
Best Local Similarity 21.2%; Pred. No. 1.7e-26;  
Matches 206; Conservative 156; Mismatches 320; Indels 290; Gaps 50;

QY 17 LCLLIA-----SPH---LQGVAGRPDELHIGFPIAGKGGWGGQAC----- 57  
Db 24 LLCVLAARQAQEMAPHSIRIEGDVT-----LGLFPVHAKG--PSGVPCGDIKREN 74  
QY 58 ---MPATRLADDVNKPNLLPGFKL---LL-----HNSDS 87  
Db 75 GIHRELAWLALDQINSNDPLPNVTLGARLTCSRDTYALEQSLTFVQALIKDTSV 134  
QY 88 ECEPGLGASVMNLYNKPQKMLLAGC--STVCTTVAEAAKMNWLVLCYGCASSPALS 145  
Db 135 RCTNGEPP-----VFVKPVGVIGAGSSVSTWANIILRLQIQISASTAPELSD 188  
QY 146 KRREPTLFRTHPSATVNPTRIKLMKFGWSRVAILOQAEVFIISTVEDLENRCWEAGE 205  
Db 189 DRRYDFRSVVPPDSFQAQAVDIVKALGMN-----YVSTLAS-EGSYGEKGE 236  
QY 206 IVTRQSLSDPTDAVRNL---RQDA-----RIIVGLVYVVAARRVLC-----EMYKQOL 252  
Db 237 SFTQISKEAGGICIAQSVRIPOERKDRITDPRDIKQLDTPNSRAVVFANDEDIKQIL 296  
QY 253 YG--RA-HVWFFIGWYEDNW-----YEVLKAEGITCTVEQMRIAAEG---HLTTEAL 299  
Db 297 AAARADQVGHFLWVSDSGSKINPLHQHEDIAEG-AITIQKRAVTEGFDAYFTSRTL 355  
QY 300 -----MW-----NONNOTTISGMTAEF-RHRLNQALIEEGYDINHDPYEGYQAP 345  
Db 356 ENNRNVWFAEYWEENFNCKLTISGSKKEDTDRKCTGQERI--GKDSNYEQ--EG--KVQ 409  
QY 346 LAYDAVWSVALAFNKTMERLTT-----GKSLRDTFTYDKEIADEIYAAMNS 392  
Db 410 FVIDAVYAMAHALHMHNMKDCADYRGVCPMEQAGGKLLKYIRHVN----- 456  
QY 393 TQFLGVSGV-VAFSSQDRIALTQIEQMDGKYKGLGYDTQDNLWS-----L 440  
Db 457 --FNGSAGTPVFNKNGD-----APGRYDIFQYQTNTNPGYRLIGQWTDLQL 504  
QY 441 NTE--QWIGG--KVQ-----DRTIVTH-- 459  
Db 505 NIEDMQMGKGVREIPSSVCTLPCKPQRRKTKGTGCCWTCPCDGYQYQFDEMTQCHP 564  
QY 460 -----VLRT-----VSLPLFCMCTISSCGIFVAFALIFNINWKKRR 497  
Db 565 YDQRPENRTGCONIPDIKLEWHSWAVIPVFLAMLGIIAT-IFVMTATFIRN-----DTP 619  
QY 498 VIQSHRPVNTIMLFGVILICLSVILLGIDGRFVSPEEYPKICQARAWLLSTGFTLAYGA 557  
Db 620 IVRASGRELSSVLLTGIFLCYIITFLM-----IAKPD--VAVCSFRVFLGLCMCISYAA 672



QY 558 MFSKVRVHRFTTKAK---TDPKKVEPWKLYTMVSGLLSIDIVILLSHQIFDPLQRYLE 614  
 Db 673 LITKTNRIYRIFEQGKSVTAP-RLISPTSQLAITSSLSVQLLVFHWFGVDPNIIID 731  
 QY 615 TFPLEDPVSTDDIKIRPELEHCEQSQRNSMWGLVYGFGLILVFLFLAYETRSIKVKQ 674  
 Db 732 ----YDEHKTMPNQARGVLK-CDITDLOIICSL--GYSILLMVTCTVVAIKTRGVP-EN 783  
 QY 675 INDSRYVGMISYNNVVVLCITAPVGMVIAEQDASFAFV-----ALAVIFCCFLSMLLI 729  
 Db 784 FNEAKPIGFTMYTTCIVWLAFIPI--FFGTAQSAEKLYIQTTTLTISMNLSASVALGMLY 841  
 QY 730 VPKVIEVIRHPKDKAESKYNPDSSAISKEDEERYQKLVTEQORLITQKEKIRVLROR 789  
 Db 842 MPKVYIIIFHPELNVQKR-----KRSFKAVVTAATMSSRLSHKPSDR----- 883  
 QY 790 LVERGDAKGTTEL 801  
 Db 884 --PNGEAK-TEL 892  
 RESULT 11  
 US-08-176-401B-2  
 ; Sequence 2, Application US/08176401B  
 ; Patent No. 6274330  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Segerson, Thomas P.  
 ; APPLICANT: Kinzie, J. Mark  
 ; APPLICANT: Mulvihill, Eileen R.  
 ; APPLICANT: Saugstad, Julie A.  
 ; APPLICANT: Westbrook, Gary L.  
 ; TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, 8th Floor  
 ; CITY: San Francisco  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA: US/08/176,401B  
 ; FILING DATE: 30-DECEMBER-1993  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Parmelee, Steven W.  
 ; REGISTRATION NUMBER: 31,990  
 ; REFERENCE/DOCKET NUMBER: 13952-18-2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 206-467-9600  
 ; TELEFAX: 415-576-0300  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 915 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-176-401B-2

Query Match 8.1%; Score 353; DB 4; Length 915;  
 Best Local Similarity 21.2%; Pred. No. 1.7e-26;  
 Matches 206; Conservative 156; Mismatches 320; Indels 290; Gaps 50;  
 QY 17 LCLLIA-----SPH---LQGVAGRPDELHIGGIFPIAGKGGWGGQAC----- 57  
 Db 24 LLCVLAAGAAGMAYPHSIRIEGVDV-----LGLLFPVHAKG--PSGVPCGDKIKREN 74

QY 58 ---MPATRLALDDVKNQPNLLPGFKL---IL-----HSNDS 87  
 Db 75 GIHRLAMUYALDQIINSDPNLLPNVTLGARILDTCSBDTYALEQSLTFVQALTKQDTSV 134  
 QY 88 ECEPGLGASVYNNLLNKPQKMLLAGC--STVCTTVAEAAKMMNLLNVLVCYGASSPALSD 145  
 Db 135 RCTNGEPP-----VFVKPEKVVGVIGAGSSSVIMVANILRLFOIPQIYSTAPELSD 188  
 QY 146 RKREPTLFRTHPSATVHNPTRIKLMKFGMSRVAILQOAAEEVFISTVEDLENRMEAGVE 205  
 Db 189 DRRYDFRSRVVPPDSFOQAAMVDIVKALGN-----YVSTLAS-EGSYGEGKVE 236  
 QY 206 IVTRQSFSLDPTDAVNR--RQDA-----RIIVGLFVYVAARRVLC-----EMYKQOL 252  
 Db 237 SFTQISKEAGGLCIAOSVRIPQERKDRITDFRIIKOLLDTPNRSRAVVIFANDEDIKQIL 296  
 QY 253 YG--RA-HWVFFIGWYEDNW-----YEVNLKAEGITCTVEQMRIAEG---HLITEAL 299  
 Db 297 AAARADQVGHFLWVGSDSGSKINPLHQHEDIAEG-AITIQPKRAVEGFDAYFTSRTL 355  
 QY 300 -----MW-----NONNOTTISGMTAEF-RHRLNOALIEGYDINHRYPEGYOEP 345  
 Db 356 ENNRNVWFAEYWEENFNCCLTISGSKEDTDKCTQGERI--GKDSNYEQ--EG--KVQ 409  
 QY 346 LAYDAVMSVALAFNKTMERLTT-----GKSLRDFTYTDKEIADEIYAMNS 392  
 Db 410 FVIDAVYMAHALHMMNKDLCADYRGVCPMEQAAGGKKLLKYIRHVN----- 456  
 QY 393 TQFLGVSGV-VAFSSOGDRIALTQIEQMIDGKYEKLYYDTQDLNLSW-----L 440  
 Db 457 --FNGSAGTVPFNKNGD-----APGRYDIFQYQTTNTNPGYRLIGOWTDELQ 504  
 QY 441 NTE--QWIGG--KVPO-----DRTIVTH-- 459  
 Db 505 NIEDMONGKVGREIPSSVCTLPCKPGQRKKTQGTGTCPCDGVQYQFDEMTCOHP 564  
 QY 460 -----VLRT-----VSLPLFVCMCTISSCGIFVAFALIFINWKKHRR 497  
 Db 565 YDORPNENRTGCONIPIIKLEHSPWNAVIPVFLAMGLIAT-IFVMATFIRYN----DTP 619  
 QY 498 VIOSSHPVCMNTIMFGVYICLISVILLGIDGRFVSPPEYKPCOARAWLLSTGFTLAYGA 557  
 Db 620 IVRASGRELISVLLTGIFLCYIITFLM-----IAKPD--VAVCSFRVFLGLGMCISYAA 672  
 QY 558 MFSKVRVHRFTTKAK---TDPKKVEPWKLYTMVSGLLSIDIVILLSHQIFDPLQRYLE 614  
 Db 673 LITKTNRIYRIFEQGKSVTAP-RLISPTSQLAITSSLSVQLLVFHWFGVDPNIIID 731  
 QY 615 TFPLEDPVSTDDIKIRPELEHCEQSQRNSMWGLVYGFGLILVFLFLAYETRSIKVKQ 674  
 Db 732 ----YDEHKTMPNQARGVLK-CDITDLOIICSL--GYSILLMVTCTVVAIKTRGVP-EN 783  
 QY 675 INDSRYVGMISYNNVVVLCITAPVGMVIAEQDASFAFV-----ALAVIFCCFLSMLLI 729  
 Db 784 FNEAKPIGFTMYTTCIVWLAFIPI--FFGTAQSAEKLYIQTTTLTISMNLSASVALGMLY 841  
 QY 730 VPKVIEVIRHPKDKAESKYNPDSSAISKEDEERYQKLVTEQORLITQKEKIRVLROR 789  
 Db 842 MPKVYIIIFHPELNVQKR-----KRSFKAVVTAATMSSRLSHKPSDR----- 883  
 QY 790 LVERGDAKGTTEL 801  
 Db 884 --PNGEAK-TEL 892

RESULT 12  
 PCT-US94-14989-2  
 ; Sequence 2, Application PC/TUS9414989  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS  
 ; NUMBER OF SEQUENCES: 3  
 ; COMPUTER READABLE FORM:



TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US91-09422-19

Query Match 8.0%; Score 349.5; DB 5; Length 912;  
Best Local Similarity 18.9%; Pred. No. 3.7e-26;  
Matches 177; Conservative 165; Mismatches 372; Indels 223; Gaps 37;

Qy 5 MTSQAVTFW--IFLLCLTIAS-----PHLOGGVAGRP-----DELHIGGIFPIAGK 48  
Db 1 MSGKGGNAWAWARUPLCLLLSLYAPWVSSLGKPKGHPHMSIRIDGDTLGLGFPVHGR 60  
Qy 49 GWWGGQAC-----MPATRLALDDVNKQPNLLPGFKL-----80  
Db 61 G--SEGKACGELKKEGHRLEAMLFALDRINNDPDLNITLGLARILDTCSRDTHALBQ 118  
Qy 81 -----ILHNSDSCEPG--LCASVMYNNLLYNNKPKMLLAGC--STVCTTVAEAAKMN 130  
Db 119 SLTFVRLIEKDGTEVRCRRGPPII-----TKPVRVGVIGASGSSVIMVANILRLFK 173  
Qy 131 LIVLCYGASSPALSDRKRFPTLFRTHPSATVHNPTRIKMKFGWSRVAIL-----QQ 183  
Db 174 IPOISYASTADLSDNSRYDFESRVVPSDTYQAQAMVDIVRAKWNVSTLASESGYGES 233  
Qy 184 ABEVFISTVEDLENRCMAGVEIVTRQSFSLSDPTDAVRLNRQDARIIVGLFYVVAARV 243  
Db 234 GVEAFIQKSRENGGVCIAQSVKIPREPKTGEDFKIKRLLETNSARGIIFANEDDIRV 293  
Qy 244 LCENYKQOLYGAHWFFIGYEDNW-----YEVNKAEG--TCTVQEMRIAEGHLT 295  
Db 294 LEAARRANQTGH---FFWMG--SDSWGSKSAPVLRLVEEVAEGAVTILPKRMSVRGFDRYF 348  
Qy 296 TEALMWNQNTTISGMTAEERHRLNQAALLEEGYDI---NHDRYPE--GYQE---APL 346  
Db 349 SSRDLNRRNIWFAEFWEDHFCKLSRALKKSHIKKCNRRERIGQDSAYEQEGKQVF 408  
Qy 347 AYDAVSVYALAFNKTMRLLTGKSLRDTFTYDKEDIADEIYAAMNSTQFLVSG--VWAFS 405  
Db 409 VIDAVYANGHALHAMRDLCPGRVCL--CPRMDPVDGTQLLKYIRNVNFSGIAGNPVTN 466  
Qy 406 SQGRIALTQIEQMDGKYELGYDYDTOLDN-----LSW-----LNTQWIGKV 450  
Db 467 ENGDI-----APGRYD---IYQQLRNGSAEYKVGISWTDLHLRIERMQWPGSQ 513  
Qy 451 PQDRTIYV-----HVLRT-----463  
Db 514 QLPRISCLPCQGERKKTVMKMACCHCEPCTGYQYQVDRTYCTCTPYDMRPTENRTSC 573  
Qy 464 -----VSLPLFCMCTISSCGIFVAFALIIFNINWKNHRRVIOSSHPCVNTI 509  
Db 574 QPIPIVKLEWDSPAVPLFLAVVGIAT-LFVVVTFVRYN-----DTPIVKASGRELSV 628  
Qy 510 MLFGVITCLISVILLIGDGRVSPPEYKPKICQARAWLLSTGFTLAYGAMFSKWVRHRT 569  
Db 629 LLAGIFLCYATFLM-----IAEPD--LGTCSLRIRFLGLGMSISYAAALLTKNRIYRF 681  
Qy 570 TKAK--TDPKKKVPWKLYTWVSGLLSIDLILLISQWFDPLQRYLEFPEDPVSSTDD 627  
Db 682 EQGRSVSAPRFTSPASQALATFTLISLQLLIGICVWFVYVDFSHVVD---FQD--QRTID 736  
Qy 628 IKIRPELHESQNSMNLGVYFGKGLILVGLFLAYETRSIKVKQINDSRVYCMISYN 687  
Db 737 PRFARGVLKCDI--SDLSLCLLGYSMLLAMTCTVYALTKRGVP--ETNEAKPIGFTMT 793  
Qy 688 VVWLCLITAPVGMVIAQQDASAFV-----ALAVIFCCFLSMILLIFPKVIEVIRHPKD 742  
Db 794 TCIWLAFIPI--FFGISQSAKLYIQTTTLTVSVLSASYSGLMYPKYIILLFHEPQ 851  
Qy 743 KAESKYNPDSAISKEDEERYOKLVTEBQRLQRLITQK 779  
Db 852 NVPKR-----KRSLKAVVTAATMSNKFTQK 876

RESULT 14  
US-08-072-574-6  
Sequence 6, Application US/08072574  
Patent No. 5521297  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen  
APPLICANT: Pontsler, Aaron  
TITLE OF INVENTION: HUMAN MATABOTROPIC GLUTAMATE RECEPTORS,  
NUCLEIC ACIDS ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 00719  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/072,574  
FILING DATE: 19930604  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 213-622-7700  
TELEFAX: 213-489-4210  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 879 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-072-574-6

Query Match 7.5%; Score 328; DB 1; Length 879;  
Best Local Similarity 20.1%; Pred. No. 5.5e-24;  
Matches 175; Conservative 134; Mismatches 320; Indels 242; Gaps 36;

Qy 36 ELHIGGIFPIAGKGGWGOAC-----MPATRLALDDVNKQPNLLPGFKLILHS 84  
Db 38 DLVLGGLFPINEKG--TGTECGRINEDRGIOLEAMLFAIDEINKDDYLLPGVKLGVHI 95  
Qy 85 NDS-----ECPGGLGASVMYNNLLYNNKPKMLLAGC--115  
Db 96 LDTCSRDTYALBQSLFVFRASLTKVDEAYMCPDG-----SYAIQENIP---LLIAGVIG 147  
Qy 116 ---STVCTTVAEAAKMNLIIVLCYGASSPALSDRKRFPTLFRTHPSATVHNPTRIKMK 172  
Db 148 GSYSSVISQVANNLLRLFQIPQISYASTSAKLSKSDYFARTVPPDFYQAKAMAILRF 207  
Qy 173 FGWSRVAILQAAEEVFISVDELE-----NRCMEAGVELVTRQSFSLSDPTDAVRN-LRR 225  
Db 208 FNTVSTVTSVASEGDYGETGIEAFEQEARLNICI-ATAEKVGRSNIRKSYSDSVIRELLOK 266  
Qy 226 QDARIIVGLFVVVAARVRVLCENYKQOLYGRAHWFFIGWY-EDNW--YEVNKAEG-----277  
Db 267 PHARVVVLFMRSDDSRELAAA-----SRANASF--TWVASDQWGAQESIINGSEHVAY 318  
Qy 278 -GITCTVEQMRTAAEGHLLTTEALMWNQNTTISGMTAEFR-----HRLNQAILEGYD 331  
Db 319 GDITLELASQPVRFGRYFQSLNPYNNHRNPWFDFWEQKFCQSLQNKRNHRRVCEKHLA 378

QY 332 INHDPYEGYQAPLAY--DAVWSVALAFNKTMERL---TT-----GKKSURDE- 375  
Db 379 IDSSNYE---QESKIMFVNNAVYAMAHALKMQRTLCPTNTTKLCDAMKILDGKKLYKDYL 435  
QY 376 -----TYTDKEIADEI-----YAAMNSTOFLGYSVVAFSSQG----- 408  
Db 436 LKINFTAFPNPKDADSVKFTDFGDMGRYNVFNQVGGKYSYLKVGHWAEITSLDVN 495  
QY 409 -----DRIALTQIEQMIDG-----KYEKL----- 427  
Db 496 SIHWSRNSVPTSCQSDPCAPNEMKNMOPGDVCCWICIPCPEYELADEFTCMDCSGQWP 555  
QY 428 ----GYDTQDNLNLSWLTQEWIGKVPQDRTIVTHVLRVTSPLFVCMCTISSCGIFV 482  
Db 556 TADLTGCDLPEDYIRW--EDAWAIGPV-----TIACIGFMCTC----- 592  
QY 483 AFALIFIINWKNHRR---VIOSSHPCVNTIMLFGVILICLISVILLGIDGRFVSPEYPKI 539  
Db 593 ----MVTVFIKHNTPLVKASGRELC-YILLFGVGLSYCMTF-----FFIAKPSPI 640  
QY 540 COARAWLSTGFTLAYGAMFSKVRVHRTTKAKTDPK--KKVEPWKLYTMVSGLLSIDL 597  
Db 641 CALRRLGLGSSFAICYSALLTKTNCIARIFDGVKNGAQRPKFTSPSSQVFCIGLILVQI 700  
QY 598 VILLSQWIFDP--LQRYL-----ETFPLEDPVSTDDIKIRPELEHCESQNSMWGLVY 650  
Db 701 VMVSWMLILEAPGTRTYLAERETVILK-----CNVKDSSMLISLT 743  
QY 651 GFKGLILVFLGLAYETRSIKVKQINDSRVGMISYVNVVLCILITAPVGMVIASQODASF 710  
Db 744 DV---ILVILCTVYAFKTRKCP-ENFNEAKFIGFTMTTCLILWLAFLPIFYVTSDDYRVQT 800  
QY 711 AFVALAVIFCCFLMLLIPVPRVIEIRHPK 741  
Db 801 FTMCIISVLSGFWVLGCLFAPKVIILFOPQ 831  
RESULT 15  
US-08-486-270-6  
; Sequence 6, Application US/08486270  
; Patent No. 5807689  
; GENERAL INFORMATION:  
; APPLICANT: Daggett, Lorrie  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Liaw, Chen  
; APPLICANT: Pontsler, Aaron  
; APPLICANT: Johnson, Edwin C.  
; APPLICANT: Hess, Stephen D.  
; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,270  
; FILING DATE: 02-JUN-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/072,574  
; FILING DATE: 04-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reiter, Stephen E.  
; REGISTRATION NUMBER: 31,192

; REFERENCE/DOCKET NUMBER: FP41 9772  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-546-4737  
; TELEFAX: 619-546-9392  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 879 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-486-270-6

Query Match 7.5%; Score 328; DB 1; Length 879;  
Best local similarity 20.1%; Pred. No. 5.5e-24;  
Matches 175; Conservative 134; Mismatches 320; Indels 242; Gaps 36;  
QY 36 ELHTGGIFPTAGGMOGQAC-----MPATRLALDDYKNQPNLPGPKLILHS 84  
Db 38 DLVIGGLFPINEKG--TGTECGRINEDRGIORLEAMLFIDEINKDDYLLPGVLGVHI 95  
QY 85 NDS-----ECEPGLGASVMYNNLYNKPQKMLLAGC-- 115  
Db 96 LDTCSRDTYALEQSLFEVFRASLTQVDEAYMCPDG-----SYAQENIP---LLIAGVIG 147  
QY 116 ---STVCTTVAEAAKMNLIVLCYGASSPALSDKRKPTFLFRTHPSATVHNPTRIKMKK 172  
Db 148 GSYSSVSIQVALLRLFOIQISYASTSAKLSKRSYDFARTVPPDFYQAKAMAEILRF 207  
QY 173 FGNRSVAILQAAEFVISTVEDLE-----NRCMEAGVEIVTRQSFSLDPTDAVN-LRR 225  
Db 208 FNMVTYVTAASEGDTGETGIEAFQEARLNICI-ATAEKVGRNIRKSYDSVIRELLQK 266  
QY 226 QDARIIVGLFYVVAARRVLCMEYKQLYGRAHVWFFIGWY-EDNW--YEVLNKAEE- 277  
Db 267 PNARVVVLFMRSDSRELIAAA-----SRANASF--TWASDNGWGAQESIIGSEHVA 318  
QY 278 -GITCTVEQMRIAAEGHLLTTEALMMNNQNTTISGMTAEFR-----HRLNOLIEBGD 331  
Db 319 GDITLELASQPVQFGRYFQSLNPNHNRNPWFDFEQKFCQSLQNRNRRVCEKHLA 378  
QY 332 INHDPYEGYQAPLAY--DAVWSVALAFNKTMERL---TT-----GKKSURDF- 375  
Db 379 IDSSNYE---QESKIMFVNNAVYAMAHALKMQRTLCPTNTTKLCDAMKILDGKKLYKDYL 435  
QY 376 -----TYTDKEIADEI-----YAAMNSTOFLGYSVVAFSSQG----- 408  
Db 436 LKINFTAFPNPKDADSVKFTDFGDMGRYNVFNQVGGKYSYLKVGHWAEITSLDVN 495  
QY 409 -----DRIALTQIEQMIDG-----KYEKL----- 427  
Db 496 SIHWSRNSVPTSCQSDPCAPNEMKNMOPGDVCCWICIPCPEYELADEFTCMDCSGQWP 555  
QY 428 ----GYDTQDNLNLSWLTQEWIGKVPQDRTIVTHVLRVTSPLFVCMCTISSCGIFV 482  
Db 556 TADLTGCDLPEDYIRW--EDAWAIGPV-----TIACIGFMCTC----- 592  
QY 483 AFALIFIINWKNHRR---VIOSSHPCVNTIMLFGVILICLISVILLGIDGRFVSPEYPKI 539  
Db 593 ----MVTVFIKHNTPLVKASGRELC-YILLFGVGLSYCMTF-----FFIAKPSPI 640  
QY 540 COARAWLSTGFTLAYGAMFSKVRVHRTTKAKTDPK--KKVEPWKLYTMVSGLLSIDL 597  
Db 641 CALRRLGLGSSFAICYSALLTKTNCIARIFDGVKNGAQRPKFTSPSSQVFCIGLILVQI 700  
QY 598 VILLSQWIFDP--LQRYL-----ETFPLEDPVSTDDIKIRPELEHCESQNSMWGLVY 650  
Db 701 VMVSWMLILEAPGTRTYLAERETVILK-----CNVKDSSMLISLT 743  
QY 651 GFKGLILVFLGLAYETRSIKVKQINDSRVGMISYVNVVLCILITAPVGMVIASQODASF 710  
Db 744 DV---ILVILCTVYAFKTRKCP-ENFNEAKFIGFTMTTCLILWLAFLPIFYVTSDDYRVQT 800

QY 711 AFVALAVIFCCFSLMLLIFVPKVIEWIRHPK 741  
Db 801 TTMCISSVLSGFWVLGCLFAPKVHILLFPQ 831

Search completed: April 30, 2002, 10:12:32  
Job time: 209 sec

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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:10:58 ; Search time 27.28 Seconds  
(without alignments)  
2280.849 Million cell updates/sec

Title: US-09-715-962-2  
Perfect score: 4374  
Sequence: 1 MKRDMTSDGAVTFWIFLCL.....LINSASHATPAATLAIQTGE 840

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
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21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	4374	100.0	840	22	AAB86159 D. melanogaster GA
2	2035	46.5	844	19	AAW40119 Human GABA-BR1b re
3	2035	46.5	844	20	AAW28839 Human GABABR1b rec
4	2035	46.5	844	20	AAW14102 Human GABAB recept
5	2035	46.5	844	21	AAV32467 Human G-protein co
6	2034.5	46.5	899	20	AAW14107 Human GABAB recept
7	2032	46.5	844	19	AAW40118 Rat GABA-BR1b rece
8	2031.5	46.4	964	20	AAW14105 Canine GABAB recept
9	2030.5	46.4	960	21	AAW83145 Human GABAB1AA rec
10	2030.5	46.4	961	20	AAV28838 Human GABABR1a rec
11	2030.5	46.4	961	20	AAV29798 Human gamma-amino-

12	2030.5	46.4	961	20	AAW14101 Human GABAB recept
13	2030.5	46.4	1323	20	AAW49133 GABA-BR1a*Gqo5 fus
14	2029.5	46.4	793	19	AAW40117 Human GABA-BR1a/b
15	2029.5	46.4	890	20	AAW14109 Human GABAB recept
16	2029.5	46.4	960	19	AAW40116 Rat GABA-BR1a rece
17	2029	46.4	962	22	AAW50090 Human GABA-B-Rla.
18	2028.5	46.4	960	20	AAW29797 Murine gamma-amino
19	2026	46.3	844	20	AAW28842 Rat GABABR1b recep
20	2026	46.3	844	20	AAW49123 Rat GABABR1a prote
21	2023.5	46.3	960	20	AAW28841 Rat GABABR1a prote
22	2023.5	46.3	960	20	AAW49122 Rat GABABR1a prote
23	2023.5	46.3	960	22	AAW50089 Murine GABA-B-Rla.
24	1967	45.0	886	20	AAW14110 Human GABAB recept
25	1721	39.3	753	22	AAW50093 GBI protein. Caen
26	1290	29.5	941	21	AAW90938 Human gamma-amino-
27	1290	29.5	941	21	AAW90938 Human GABA-B recep
28	1290	29.5	941	21	AAW51928 Human GABA-B recep
29	1290	29.5	941	21	AAW70328 Human GABA-B-R2 re
30	1290	29.5	941	21	AAW79202 Human GABAB recept
31	1290	29.5	941	21	AAW44342 Human gb2 GABA B r
32	1290	29.5	941	22	AAW50088 HG20 protein seque
33	1290	29.5	943	20	AAW28837 Human GABABR2 rece
34	1289	29.5	941	21	AAW68743 A human gamma-amino
35	1287	29.4	940	21	AAW44343 Rat gb2 GABA B rec
36	1285.5	29.4	914	21	AAW44344 Protein-1 related
37	1285.5	29.4	965	21	AAW44345 Protein-2 related
38	1285	29.4	1303	20	AAW49132 GABA-BR2*Gqo5 fusi
39	1284	29.4	898	20	AAW14082 Human GABABR2 prot
40	1284	29.4	898	21	AAW70326 Human gamma amino
41	1283	29.3	940	21	AAW90937 Rat GABA-B recepto
42	1283	29.3	940	21	AAW70327 Rat gamma amino bu
43	1282	29.3	940	21	AAW51927 Rat GABA-B recepto
44	1263	28.9	883	20	AAW14081 Rat GABABR2 protei
45	1249.5	28.6	473	20	AAW49107 Human GABABR1b ext

#### ALIGNMENTS

RESULT 1  
AAB86159  
ID AAB86159 standard; Protein; 840 AA.  
XX AC AAB86159;  
XX AC AAB86159;  
DT 03-AUG-2001 (first entry)  
XX D. melanogaster GABA-B receptor protein SEQ ID 2.  
DE GABA-B receptor; fruitfly; gamma-aminobutyric acid B receptor;  
KW insecticide; transgenic invertebrate; plant protection agent;  
KW human medicine; veterinary medicine; insect.  
XX Drosophila melanogaster.  
XX DE19955408-A1.  
XX 23-MAY-2001.  
PD 18-NOV-1999; 99DE-1055408.  
PF 18-NOV-1999; 99DE-1055408.  
PR 18-NOV-1999; 99DE-1055408.  
XX (FARB ) BAYER AG.  
XX Raming K, Mezler M, Mueller T;  
XX WPI; 2001-318282/34.  
XX N-PSDB; AAH20519.  
XX New invertebrate gamma-aminobutyric acid receptor proteins, useful in  
XX screening for potential insecticides, for plant protection or medicine,  
XX also related nucleic acid

XX Claim 2; Page 16-21; 62pp; German.  
XX This invention describes a novel polypeptide (I), functioning as a  
CC gamma-aminobutyric acid -B (GABA-B) receptor which has insecticidal  
CC activity. (I), also the nucleic acid (II) that encodes it and related  
CC vectors, host cells, antibodies and transgenic invertebrates, are used  
CC for identifying: (i) new plant protection agents, i.e. modulators of (I)  
CC with insecticidal activity, which may also be useful in human or  
CC veterinary medicine; and (ii) genes that encode polypeptides involved in  
CC assembly of functionally related GABA-B receptors in insects. This  
CC sequence represents a fruitfly (Drosophila melanogaster) GABA-B receptor  
CC which is described in the method of the invention.  
XX  
XX Sequence 840 AA;  
XX  
Query Match 100.0%; Score 4374; DB 22; Length 840;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRKDMTSDGAVTFWIFLLCLLIASPHLQGGVAGRPDELHIGGIFPIAGKGWGGQACMPA 60  
DB 1 mrkdmtsdgavtfwifllclliasp hlggvgagrpdelhiggi fpiagkgwggqacmpa 60  
QY 61 TRIALDDVNKQPNLLPGFKLILHSNDECEPGLGASVWYLLNKPOKLMLLAGCSTVCT 120  
DB 61 trialddvnkqpnllpgfk lilhnsndec epglgasvwyllnkp oklml laggcstvtct 120  
QY 121 TVAEAAKMNLLIVLCYGASSPALSDRKRPFLRTPHPSATVHNPTRIKLMKFCGWSVAI 180  
DB 121 tvaeaa kmnllivlc ygasspal sdrk rpf lrtphpsatv hnp tr iklmk fcgwsvai 180  
QY 181 LQAQEEVFISTVEDLENRCMEAGVEIVTRQSFSLSDPTDAVRNLRRODARIIVGLFYVAA 240  
DB 181 lqaqeevfistvedlenrc meagveivtrq sfslsdptd avrn lrr o d ariivglfyvaa 240  
QY 241 RRVLCMEYKQQLYGRAHWFYFIQWEDNMYEVNKLKAGITCTVEQMRFAAEGHLLTTEALM 300  
DB 241 rrvlcme ykql ygrahwfyfiqw ednmyevnkl kagitctve qmrfaa eghllttealm 300  
QY 301 WQNNQTTISGMTAEERFRLHNOALTEEGYDINHDPYECYQAPLAYDAVSWALAFNK 360  
DB 301 wqnnqt tismgt aeerf rhlhnoal teegy dindh dpyecy qaplayd avswalafnk 360  
QY 361 TMERLTGKSLRDFYTTDKEDIAEYAAAMNSTQFLGCVSGVAFSSOGDRIALTQIEQMI 420  
DB 361 tmerltg kslrdfy ttdkediae yaaamnstq flgcvsgvaf ssgdr ialtqieqmi 420  
QY 421 DGKYEKLYDYTDLDNLISWNTQEWIGGKVPQDRTIVTHVLRVSLPLFVCMCTISSCGI 480  
DB 421 dgkyekly dytdldnl iswntq ewiggkv p qdrtiv thvlrv slplfvc mctisscgi 480  
QY 481 FVAFALIIENWKNHRRVIOSSHPVCNTIMLFGVILCLISVILLIGIDGRFVSPEEYKIC 540  
DB 481 fvafal iienwkn hrrv ioss h pvcntim lfgvil clisv illig idgrfvs pee ykic 540  
QY 541 QARAWLLSTGFTLAYGAMFSGKVRVHRTTKAKTDPKKVPKWLTYMTWSGLLIDIVIL 600  
DB 541 qarawl l stgft layg amfsgkvr vhr ttkak tdpkkvpk wlymtws gl lidiv il 600  
QY 601 LSWQIFDPLQRYLETPLFDPVSTDDIKIRPELEHESQSNMWSGLVGFSGKLILVFG 660  
DB 601 lswqifd plqry letpl fdpv stddi kirpelehes qsnm wsglv g fsgklilvfg 660  
QY 661 LFLAYETRSIKVKQINDSRVGSYINVVVLCITAPVGMVIAQQDASFAVALAVIFC 720  
DB 661 lflayetr sikvkq indsr vgsy invvv lc itapvgmv iasqqd asfafvalavifc 720  
QY 721 CFLSMILLIFVPKVIEWIRHPKDAESKYNPDPSAISKEDEERYQKLVTENEOQLRLITQKE 780  
DB 721 cflsmill ifvpk vieir hpkda eskynp dpsaisk edeery qklvt eneoqlrlitqke 780

QY 781 EKIRVLQRILVERGDAGKTELNGATGVASAAVATTTSQPASLINSSAHATPAATLAIQTGE 840  
DB 781 ekirvlqrilvergdagk telngatgv asaa vat t t s q p a s l i n s s a h a t p a a t l a i q t g e 840  
RESULT 2  
AAW40119  
ID AAW40119 standard; Protein; 844 AA.  
XX AAW40119;  
AC AAW40119;  
XX 03-JUN-1998 (first entry)  
DT Human GABA-BR1b receptor protein.  
DE  
XX Gamma-aminobutyric acid; GABA-BR1a/b receptor; human; brain; agonist;  
KW inhibitory neurotransmitter; peripheral nervous system; antagonist;  
KW treatment; dementia; depression; anxiety; bronchial inflammation; asthma;  
KW epilepsy; cognitive function.  
XX Homo sapiens.  
OS  
XX WO9746675-A1.  
PN  
XX  
XX 11-DEC-1997.  
PD  
XX 19-MAR-1997; 97WO-EP01370.  
PF  
XX 22-NOV-1996; 96US-0756091.  
PR 30-MAY-1996; 96US-0655716.  
XX  
XX (NOVS ) NOVARTIS AG.  
PA  
XX Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;  
PI WPT; 1998-042183/04.  
XX N-PSDB; AAV10267.  
DR  
XX Purified GABA-B receptor or receptor protein - and antagonists of  
PT these which may be useful in treating nervous system disorders  
PT  
XX Claim 4; Page 86-90; 108pp; English.  
PS  
XX This sequence represents a novel human GABA-B receptor protein,  
CC GABA-BR1b. GABA (gamma-aminobutyric acid) is the major inhibitory  
CC neurotransmitter found in the brain and peripheral nervous system  
CC and this receptor may be used for the identification of GABA-B  
CC receptor agonists and antagonists. Such proteins may be used in  
CC treatment of dementia, depression, anxiety, epilepsy, spasticity,  
CC bronchial inflammation or asthma or to improve cognitive function.  
CC GABA-B receptor ligands and probes derived from this sequence can be  
CC used to assay for GABA-B receptors or DNA encoding them.  
XX  
XX Sequence 844 AA;  
XX  
Query Match 46.5%; Score 2035; DB 19; Length 844;  
Best Local Similarity 49.3%; Pred. No. 7,5e-193;  
Matches 387; Conservative 151; Mismatches 219; Indels 28; Gaps 9;  
QY 23 SPHL---GGVAGRDE----LHIGGIFPIAGKGWGGQACMPATRIALDDVNKPNLL 75  
DB 23 sphlprphsrpphpserravvialgfpms--ggwpqgqacqpavema ledvnsrrdl 89  
QY 76 PGFKLILHSNDECEPGLGASVWYLLNKPOKLMLLAGCSTVCTVTAQAAKMNLLIVLC 135  
DB 76 pgyelklilhds kcdpgqatkylyell yndpikilmpgcssvstlv aeaarmnllivs 149  
QY 136 YGASSPALSDRKRPFLRTPHPSATVHNPTRIKLMKFCGWSRVAILLQAAEEVFISTVEDL 195  
DB 150 ygasspal sdrk rpf lrtphpsatv hnp tr iklmk fcgwsrvail lqaaeevfistvedl 209  
QY 196 ENRCMEAGVEIVTRQSFSLSDPTDAVRNLRRODARIIVGLFYVVAARRVLCMEYKQQLYGR 255

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Db 210 eervkeagieitfrdgsfddpavpknkrqdarlivgifyetearkvfveykerlfgk 269
Qy 256 AHVFFIGWYEDNWYEVNKAEGITVEOMRIAAEGHLTTEALMWNQNNOTTISGMTAE 315
Db 270 kyvfwligyadnwfk--ydpinctvdmteaveghitteivmnpantrsismntsq 327
Qy 316 EFRHRLNQAIEEGYDINHRYPE---GYOEAPLAYDAVMSVALAFNKTMRERLTGKKSL 372
Db 328 efvekitkrl-----krpheetggfqaepalaydaialalalankts999grsgvrl 378
Qy 373 RDTYTDKEIADEIYAAMNSTQFLGVGVVAFSSQGDRIALTOIEQMIDGKYEKLGYYDT 432
Db 379 edfnynnqtdtdqiyramnsssfegsvghvfdasgrmawtlieqlggysykkigyds 438
Qy 433 OLDNLNWLNTQEWIGGKVPQDRITVTHVLTSLPLFVCMCTISSGIFVAFALIFFNW 492
Db 439 tkddlswwktkwggsppadtvlktfrflsqklfsvslslgvlavvcfsfnly 498
Qy 493 NKHRRVIOSSHVPVCNTIMLFGVVIICLISVILLGIDGRFVSPPEYPKICQARAWLLSTGFT 552
Db 499 nshvryiqnsqpnlnltavgcsalaaavfplgldgyhigrnqpfvcqarlwlglgfs 558
Qy 553 LAYGAMFSKVVRVHREFTK--AKTDPKKKVEPKWLYTWVSGLLSIDLVLLSWQIFDPLQ 610
Db 559 lgygsmftkiwwhtvftkkekewrktlepklyatvgllvgnmdvltaiwqivdplh 618
Qy 611 RYLETFFLEDVSTDDIKIRPELECHESORNMSWGLVYGVKGLIILVFLGFLAYETRSL 670
Db 619 rtietfakeepkedi-dvslilpglehcsrrkmtwlgfygkglillilgflayetsk 677
Qy 671 KVKQINDSRVYGVMSIYVNVVLCITAPVGVVIASQODASFAFVALAVIFCCFLSMILLIFV 730
Db 731 PKVIEVIRHP--KKAESKYNPDSAISREDERYOKLVNTENQOLRLITQKEEKIRVLQ 788
Db 738 pkmrllitrgewqseqadtmtgssstnnneeksrllekenrelekiiaekeervselh 797
Qy 789 RLVER 793
Db 798 qlqr 802

RESULT 3
ID AAY28839 standard; Protein; 844 AA.
AC AAY28839;
XX
XX
XX 17-JAN-2000 (first entry)
DE Human GABABR1b receptor protein.
XX
KW GABABR1b receptor protein; cloning; rat brain; GABABR2; GABAB receptor;
KW human gamma-aminobutyric acid receptor; metabotropic receptor; screening;
KW synaptic transmission; GABABR1b; cloned receptor; splice variant;
KW modulatory agent; molecular activity assay; anisipastic; anti-addictive;
KW antineurodegeneration; analgesic; cardiovascular activity.
XX
OS Homo sapiens.
XX
XX WO9951636-A2.
XX
XX 14-OCT-1999.
XX
XX 02-APR-1999; 99WO-US07352.
XX
XX 03-APR-1998; 98US-0080676.
XX
XX (NPS-) NPS PHARM INC.
XX
XX Garrett JE, Simin RT, Busby JG, Stormann TM;

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XX
DR WPI; 1999-610994/52.
DR N-PSDB; AAX90921.
XX
PT Novel nucleic acids, used to screen for specific modulators, e.g. for
PT treating spasticity or Alzheimer's disease
XX
PS Disclosure; Fig 2A-2E; 78pp; English.
XX
XX The present sequence encodes GABABR1b receptor protein cloned from rat
CC brain. This is closely related to GABABR2. GABAB receptors are
CC metabotropic receptors that modulate synaptic transmission in brain.
CC GABABR1a differs from GABABR1b in that the N-terminal 147 residues are
CC replaced by 18 amino acids. Both of these cloned receptors appear to be
CC splice variants. They are expressed in cells that express GABABR2. This
CC nucleotide sequence is used to screen for specific modulators. These
CC modulators have antispastic, antineurodegeneration, analgesic, anti
CC -addictive, cardiovascular activities.
CC Note: SEQ ID NO. 8 is referred as the GABABR1a receptor protein in
CC the specification.
XX
XX Sequence 844 AA;
XX
Query Match 46.5%; Score 2035; DB 20; Length 844;
Best Local Similarity 49.3%; Pred. No. 7.5e-193;
Matches 387; Conservative 151; Mismatches 219; Indels 28; Gaps 9;
Qy 23 SPHL---OGVAGRPDE---LHIGGIFPIAGKGGWGGQACMPATRLALDDVKNQPNLL 75
Db 32 sphlprphsvrpphserravyigalpm--ggwpggacqpavemaiedvnrsrdil 89
Qy 76 PGFKLLIHSNDCCEPGIASVMVNLNPKOKMLLAGCTVCTTVAEAKMNLVILC 135
Db 90 pdyelkllhdsxcdp9gatkyllylndpkiilmpgcsvctlvaearmnllivs 149
Qy 136 YGASSPALSDKRFPFTLFRTHPSATVHNPTRIKLMKFGWSRVAILQAQAEVFTSTVEDL 195
Db 150 ygssspalsnqrqfptfrthpsatlhnptrvklfkgwkkkiatqgttevfstidll 209
Qy 196 ENRCMEAGVEIVTRQSFSLDPTDAVNLRRQDARIIVGLFVYVVAARRVCEMKQOYLGR 255
Db 210 eervkeagieitfrdgsfddpavpknkrqdarlivgifyetearkvfveykerlfgk 269
Qy 256 AHVFFIGWYEDNWYEVNKAEGITVEOMRIAAEGHLTTEALMWNQNNOTTISGMTAE 315
Db 270 kyvfwligyadnwfk--ydpinctvdmteaveghitteivmnpantrsismntsq 327
Qy 316 EFRHRLNQAIEEGYDINHRYPE---GYOEAPLAYDAVMSVALAFNKTMRERLTGKKSL 372
Db 328 efvekitkrl-----krpheetggfqaepalaydaialalalankts999grsgvrl 378
Qy 373 RDTYTDKEIADEIYAAMNSTQFLGVGVVAFSSQGDRIALTOIEQMIDGKYEKLGYYDT 432
Db 379 edfnynnqtdtdqiyramnsssfegsvghvfdasgrmawtlieqlggysykkigyds 438
Qy 433 OLDNLNWLNTQEWIGGKVPQDRITVTHVLTSLPLFVCMCTISSGIFVAFALIFFNW 492
Db 439 tkddlswwktkwggsppadtvlktfrflsqklfsvslslgvlavvcfsfnly 498
Qy 493 NKHRRVIOSSHVPVCNTIMLFGVVIICLISVILLGIDGRFVSPPEYPKICQARAWLLSTGFT 552
Db 499 nshvryiqnsqpnlnltavgcsalaaavfplgldgyhigrnqpfvcqarlwlglgfs 558
Qy 553 LAYGAMFSKVVRVHREFTK--AKTDPKKKVEPKWLYTWVSGLLSIDLVLLSWQIFDPLQ 610
Db 559 lgygsmftkiwwhtvftkkekewrktlepklyatvgllvgnmdvltaiwqivdplh 618
Qy 611 RYLETFFLEDVSTDDIKIRPELECHESORNMSWGLVYGVKGLIILVFLGFLAYETRSL 670
Db 619 rtietfakeepkedi-dvslilpglehcsrrkmtwlgfygkglillilgflayetsk 677
Qy 671 KVKQINDSRVYGVMSIYVNVVLCITAPVGVVIASQODASFAFVALAVIFCCFLSMILLIFV 730

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Db 678 steindhravmalyvavclitapvtmllssqdaafafaslaivfssytilvlfv 737  
QY 731 PKVIEWIRHP--KDKAESKYNPDSSAISKEDERYQKLVTEQOLRLITQKEKIRVLQ 788  
Db 738 pkmrllitrgewqseaqdmktgssstnnneeksrllenenrelekkiaeekeervselrh 797  
QY 789 RLVER 793  
Db 798 qlqsr 802

RESULT 4  
AAY14102  
ID AAY14102 standard; Protein; 844 AA.  
AC AAY14102;  
XX 21-JUL-1999 (first entry)  
XX Human GABAB receptor lb protein sequence.  
XX GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;  
KW transient lower oesophageal sphincter relaxation; spasticity; emesis;  
KW gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;  
KW irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;  
KW autoimmune disease; neoplastic disease; infectious disease; therapy.  
OS Homo sapiens.  
XX W09921890-AL.  
XX 06-MAY-1999.  
XX 27-OCT-1998; 98MO-SE01947.  
PR 17-JUL-1998; 98SE-0002575.  
PR 27-OCT-1997; 97SE-0003914.  
PR 16-MAR-1998; 98SE-0000864.  
XX (ASTR ) ASTRA AB.  
PI Ekstrand J;  
XX WPI; 1999-302985/25.  
DR N-PSDB; AAX58055.  
XX Polynucleotides encoding human and canine gamma aminobutyric acid  
PT type B receptors, used to screen for compounds that are inhibitors  
PT of transient lower oesophageal sphincter relaxations  
PS Claim 17; Page 90-94; 222pp; English.  
XX This sequence is a human gamma aminobutyric acid type B (GABAB)  
CC receptor of the invention. Nucleic acid molecules encoding GABAB  
CC receptors can be used to screen for compounds that are inhibitors of  
CC transient lower oesophageal sphincter relaxations (TLESR). They can also  
CC be used to screen for agonists or antagonists of the GABAB receptors.  
CC Inhibitors of TLESR are useful for treating gastro-oesophageal reflux  
CC disease. Other uses of GABAB receptors, such as human GABAB Ric or 1d,  
CC comprise diagnosis or treatment of conditions related to GABAB  
CC dysfunction, e.g. epilepsy, psychiatric disorders, emesis, irritable  
CC bowel syndrome, dyspepsia, spasticity, arthritis, allergies, autoimmune  
CC diseases, neoplastic diseases, pain and infectious disease.  
XX Sequence 844 AA;  
SQ

Query Match 46.5%; Score 2035; DB 20; Length 844;  
Best Local Similarity 49.3%; Pred. No. 7.5e-193;  
Matches 367; Conservative 151; Mismatches 219; Indels 28; Gaps 9;  
QY 23 SPHL---QGVAGRPE---LHIGGIFPIAGKGGWGGQACMPATRLALDDVNNKQPULL 75

Db 32 sphlprhpsrpphserravyigalifpms--ggwpggacqpavemaledvnsrrdil 89  
QY 76 PGFKLIHNSDSECEPGASQVWYNNLYNKPKQLMLLAGCTVCTTVAEAAKMNLIIVLC 135  
Db 90 pdyelkiihndskdpggatkyllyellindpikiilmpgcssvstlvaearmwnlilvs 149  
QY 136 YGASSPALSDRKREPTLFRTHPSATVHNPTRIKLMKFGWSRVALLQQAEEVFISTVEDL 195  
Db 150 ygssspalsnrqfptftrthpsatllhnptrvki fefgwkwkatiqgtteftstldl 209  
QY 196 ENRCMEAGVEIVTROSFLSDPTDAVRNLRODAIIIVFYVAARVCLCEMYKQOLYGR 255  
Db 210 eervkeagieitfrqsfdsdpavpvknkrqdarilvlgfyetearkvfcevyerlqgk 269  
QY 256 AHVWFFIGWYEDNWEYVNLKAEIGTCTVEQMRIAEGLHTTEALMWNQNNQTTISGMFAE 315  
Db 270 kywvfligwyadnwfk1--ydpnsinctvdemteaveghitteivmlnpantrsinsmtsq 327  
QY 316 EFRHRLNQAIEEGYDINHDPYPE---GYQAPLAYDAVNSVALAFNKTMERLTTGKKSL 372  
Db 328 efvekltkrl-----krhpeetggfgeaplaydaialalalnktsgggrsgvrl 378  
QY 373 RDEYTKKEIADEIYAAAMNSQFGLVSGVAFSSQGDRIALTOEOMIDGKYEKLYYDT 432  
Db 379 edfnynnqtldqlyramnsssfegvshvfdasgsrmatllleqigqgskklygyyds 438  
QY 433 QLDNLSWLNTBQWIGGKVPQDRTIVTHVLRVSLPLFCMCTISSCGIFVAFALIFNIW 492  
Db 439 tkddlsksktdkwlgsgppadtiviktrfslqklfsvslsglavlavvcslsfny 498  
QY 493 NKHRRVQSSHPVNCNTIMLFGVILISVILLGDGRVSPPEEPKICQARAWLLSTGFT 552  
Db 499 nshvryiqnsqpnlnltavgcslalaavfplgidgyhigrnqfpvqcarllwllglfs 558  
QY 553 LAYGAMFSKVMRVHRFTTK--AKTDPKKKVPWKLYTMVSGLSLDLVLLSWQIFDPLQ 610  
Db 559 lgygsmtfkliwwhtvftkkekewrktlepklyatvgllvgmdvltlatwqivdplh 618  
QY 611 RYLETFLPEDPVSTDDIKIRPELEHCSQRNMSMLGVYGFGLILVFLAYETRSL 670  
Db 619 rtietfakkepke di-dvslilpqiehcscrkmtwtlgyfygkglillilgflayetsk 677  
QY 671 KVKQINDSRVYGMISYINVVVLCLITAPVGMVIAQQDASAFVALAVIFCCFLSMLLIFV 730  
Db 678 stekindhvragmalyvavclitapvtmllssqdaafafaslaivfssytilvlfv 737  
QY 731 PKVIEWIRHP--KDKAESKYNPDSSAISKEDERYQKLVTEQOLRLITQKEKIRVLQ 788  
Db 738 pkmrllitrgewqseaqdmktgssstnnneeksrllenenrelekkiaeekeervselrh 797  
QY 789 RLVER 793  
Db 798 qlqsr 802

RESULT 5  
AAY32467  
ID AAY32467 standard; Protein; 844 AA.  
AC AAY32467;  
XX 27-MAR-2000 (first entry)  
XX Human G-protein coupled receptor GABABlb.  
XX GABABlb; G-protein coupled receptor; human; antibacterial;  
KW antiviral; virucide; antiparasitic; analgesic; cytostatic;  
KW antidiabetic; anorectic; cardiant; antiparkinsonian;  
KW hypertensive; hypotensive; antiemetic; osteopathic; antitanginal;  
KW cerebroprotective; antituler; antiallergic; neuroleptic;  
KW tranquilizer; antidepressant; nootropic; antimigraine;  
KW anticonvulsant; neuroleptic; agonist; antagonist; inhibitor;







QY 615 TFPLEDPVSTDDIKIRPELEHESORNMSWGLVYGFKGLILVFLGFLAYERSIKVKQ 674  
Db 743 trakeepkedi-dvslpqlchccskmmtwifgykgllilgflayetskystek 801  
QY 675 INDSRYVGMISYNNVVLCLITAPVGMVIAASQODASFAFVALAVIFCCFLSMLLIFVPKVI 734  
Db 802 indhravgmamynvavclitapvtmllssqdaafafaalaivfsyitlvilvfpkmr 861  
QY 735 EVIRHP--KDKAESKYNPDSAISKEDERYQKLVTEQRLQRLITQKEEKIRVLQRLVE 792  
Db 862 rliitrgewqseqdmtkgtstnnneeksrlllekenrelekiiakeervselrqlrs 921  
QY 793 R 793  
Db 922 r 922  
RESULT 9  
AY83145  
ID AY83145 standard; Protein; 960 AA.  
AC AY83145;  
DT 24-JUL-2000 (first entry)  
XX Human GABAB1AA receptor.  
XX GABAB1AA receptor; G-protein; disease; treatment; detection;  
KW therapy; antibody; immune response; infection; cancer; diabetes;  
KW obesity; anorexia; bulimia; Parkinson's disease; heart failure;  
KW hypotension; hypertension; urinary retention; osteoporosis;  
KW angina pectoris; myocardial infarction; stroke; ulcers; asthma;  
KW allergy; benign prostatic hypertrophy; migraine;  
KW neurological disorders including anxiety; schizophrenia;  
KW depression; dementia; Huntington's disease;  
KW Gilles de la Tourette's syndrome.  
XX  
OS Homo sapiens.  
XX  
XX WO200012106-A1.  
XX  
XX 09-MAR-2000.  
XX  
XX 30-AUG-1999; 99WO-US19435.  
XX  
XX 01-SEP-1998; 98US-0144779.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX Elshourbagy NA;  
XX  
XX WPI; 2000-237771/20.  
XX N-PSDB; AA293411.  
XX  
PT New GABAB1AA polypeptide useful for diagnosis, treatment and prevention  
PT of diseases associated with its expression including infections,  
PT psychotic and neurological disorders and cancer  
XX  
PS Claim 1; Page 34-36; 38pp; English.  
XX  
XX The GABAB1AA receptor is believed to be a member of the GABAB  
XX family of polypeptides. They are therefore of interest because  
XX members of the purinergic 7m receptor family (G-protein coupled  
XX receptors) of genes are involved in a number of biological and  
XX disease manifestations. They are also a successful target for  
XX pharmaceutical intervention. Antibodies directed against GABAB1AA  
XX and its peptides can be used to treat bacterial, fungal, protozoan  
XX and viral infections, pain, cancers, diabetes, obesity, anorexia,  
XX bulimia, Parkinson's disease, acute heart failure, hypotension,  
XX hypotension, urinary retention, osteoporosis, angina pectoris,  
XX myocardial infarction, stroke, ulcers, asthma, allergies, benign  
XX prostatic hypertrophy, migraine, vomiting, psychotic and  
XX neurological disorders including anxiety, schizophrenia, depression,

CC dementia and severe mental retardation and dyskinesias such as  
CC Huntington's disease or Gilles de la Tourette's syndrome. The  
CC GABAB1AA polypeptide or a vector comprising a sequence encoding the  
CC polypeptide can be used to induce an immunological response in a  
CC mammal to protect against disease. The presence or absence of a  
CC mutation in the nucleotide sequence encoding the GABAB1AA polypeptide  
CC can be detected in the genome of a subject and/or the presence or  
CC amount of expression of the polypeptide in a sample from the subject  
CC can be analysed and used to diagnose a disease or susceptibility to a  
CC disease related to the expression or activity of GABAB1AA.  
CC Diagnosis can be measured at the RNA level using nucleic acid  
CC amplification, e.g. polymerase chain reaction, RNase protection or  
CC Northern blotting or at the protein level by radioimmunoassay,  
CC competitive-binding assays, Western blot analysis or ELISA assays  
CC (enzyme linked immunosorbent assay).  
XX  
SQ Sequence 960 AA;  
Query Match 46.4%; Score 2030.5; DB 21; Length 960;  
Best Local Similarity 49.3%; Pred. No. 2.6e-192;  
Matches 384; Conservative 152; Mismatches 220; Indels 23; Gaps 8;  
QY 24 PHLQGGVAGRPDE--LHIGGIFPIAGKGGQGGQACMPATRLALDDVKNQPNLPGFKLI 81  
Db 154 phcdvnrtpshserravyigalfpms--ggwpggacgpavemaledvnsrrdlipdeik 211  
QY 82 LHSNDSCEPCGLGASVMYLNKPKLMLGACSTCTTVAEAAKMNNLVLCVGASSP 141  
Db 212 lihdsxcdp9gatykyellindpikilmpgcssvstlvaearmnnlilvsgsssp 271  
QY 142 ALSDRKRPPTLFRPHSATVHNPTRIKLMKFGMSRVAILOQAEVEFISTVEDLENRMC 201  
Db 272 alsnrqfptfrthpsatlnhptvrklfekwggkklattqgttevfstlddleervke 331  
QY 202 AGVEIVTRQSFSLDPTDAVRNLRQDARIIVGLFVVAARRVLCVEMYKQQLYGRAHWFF 261  
Db 332 agleitfrqsfspavpvnknkrqdarilvglfyetearkvfcevykerfgykvvwl 391  
QY 262 IGWYEDNWEVNKAEGITCTVEQMRIAEGHLTAEALMNNQNTTISGMTAEERHRL 321  
Db 392 igwyadhwfki--ydpnsinctvdenteaveghittetvmlnpantrsismtsqefvekl 449  
QY 322 NQALIEEGYDINHRYPE--GYQEAFLAYDAVMSVALAFNKTMRERLTGKSKSLRDTYT 378  
Db 450 tkrl-----krhpeetggfgeaplaydaialalalnktstgggrsvrledfyn 500  
QY 379 DKETADEIYAAMNSTQFLGSGVVAFFSQGDRIALTQEQMIDGKYEKLYGYYDTOLDNLS 438  
Db 501 nqtitdgiyramnsssfegvhvfdasgrmawtlieqlqggyskkygyvdstkddls 560  
QY 439 WLNTEQMTGGKVPQDRTIVTHVTRVSLPLFVCMCTISSCGIFVAFALIIENINMKHRRV 498  
Db 561 wsktdkwlg9spadqtlviktfrflsqklflfsvslssglvliavvcslfniynshvry 620  
QY 499 IQSGHPVCNTTMLFGVITCLISVILLGIDGRFVSPPEEYPKICQARAWLLSTGFTLAYGAM 558  
Db 621 ignsqpnlnltavgcslalaavfplgldghygnrqnfvcqarllwlgfslgysgm 680  
QY 559 FSKVMVRHRTTK--AKTDPKKKVEPWKLYTMVSGLLSIDLVILLSWQIFDPLQRYLETF 616  
Db 681 ftkiwwhtvtkkekewrktlepwklyatvgilvgmdvltaiwqivdphrtietf 740  
QY 617 PLEDPVSTDDIKIRPELEHESQNSWGLVYGFKGLILVFLGFLAYERSIKVKQIN 676  
Db 741 akeepkedi-dvslpqlchccskmmtwifgykgllilgflayetskystekin 799  
QY 677 DSRVVGSIYNNVVLCLITAPVGMVIAASQODASFAFVALAVIFCCFLSMLLIFVPKVI 736  
Db 800 dhravgmamynvavclitapvtmllssqdaafafaalaivfsyitlvilvfpkmr 859  
QY 737 IRHP--KDKAESKYNPDSAISKEDERYQKLVTEQRLQRLITQKEEKIRVLQRLVE 793  
Db 922 r 922



PT New DNA encoding human and murine receptor subunits, useful for  
PT identifying agonists and antagonists for treatment of depression,  
PT epilepsy and neuropsychiatric disorders  
XX  
PS Claim 11; Fig 18; 128pp; English.

XX The present sequence represents a human gamma-amino-butyric acid (GABA)  
CC B receptor (GABABR) subunit designated GABABR1a. The present invention  
CC also describes the GABABR subunit designated HG20. Cells expressing  
CC the new receptor subunits are useful for identifying GABABR agonists  
CC and antagonists. HG20 proteins and their antagonists are useful for  
CC inhibiting HG20 or GABABR function, useful for treating depression,  
CC epilepsy, neuropsychiatric disorders, dementias, muscular contractions,  
CC and central nervous system disorders.

XX Sequence 961 AA;

Query Match 46.4%; Score 2030.5; DB 20; Length 961;  
Best Local Similarity 49.3%; Pred. No. 2.6e-192;  
Matches 384; Conservative 152; Mismatches 220; Indels 23; Gaps 8;

QY 24 PHLOGGVAGRDPDE--LHIGGIFPIAGKGGWGGOGACMPATRLALDDVKNKPNLLPGFKLI 81  
DB 155 phcqvnrtpsherravvigaifpms--ggwpgggacqavemaedvnsrrdlpdyelk 212

QY 82 LHSNDECEPGLGASVYNNLLYNKPKQLMLLAGCTVCTTVAARAKMWNLLIVLCYGASSP 141  
DB 213 lihndskcdpgqatkyllyelpndpikilmpgcssvstlvaearmwnllivlysgssp 272

QY 142 ALSDRKRPTLFRTHPSATVHNPTRIKLMKKFGWSRVAILQQAEEVFISTVEDLENRCME 201  
DB 273 alsnrqrfptftrhpsatvhnptrvkfkewgwkkiatigttteftstlddleervke 332

QY 202 AGVEIVTROSEFLSDPTDVRNLRQDARIIVGLFYVVAARRVLCVCEMYKQQLYGRAHWFF 261  
DB 333 agieifrdgsfddpavpvnkrlrqdarliivfietearkvfcevyeerlfgkkywfl 392

QY 262 IGWYEDNWEVNLKAGTICTVQMRTAAGHLTTALMNQNNQTTISGMTAEPEPHRL 321  
DB 393 igwadnwfkf--ydpisinctvdeameaveghitteivmlnpantrsismtsqefvekl 450

QY 322 NOALIEEGYDINHRYPE---GYQEAFLAYDAVMSVALAFNKTMRITTTGCKSLRDFYTT 378  
DB 451 tkrl-----krhpeetggfgeaplaydaiwalalalnktsgggrsgrvrledfyn 501

QY 379 DKEIADEIYAAMNSTOFLGSGVVAVSSQGDRIALQIEQIDGKYEKLGYYDTQDNL 438  
DB 502 nqdtidqiyramnsssfegvshvfdasgrmawtlielqggyskkgiydstkdls 561

QY 439 WLNTQEWIGGKVPQDRTIVTHVLTSLPLFVCMCTISSGIFVAFALITFINWKKHRY 498  
DB 562 waktkwiggspadqtlviktfrfisklfisvsvlssigvlavvclsnfynshvry 621

QY 499 IQSSHPVCMTIMLFGVILICLISVILLGIDGRFVSPPEYPKICQARAWLLSTGFTLAYCAM 558  
DB 622 ignsqpnlnaltavgcslalaaavplgldgyhgrnqpfvcqarlwlglgfslygysm 681

QY 559 FSKWVRVHRTTK--AKTDPKKVPEWPKLYTMVSGLLSIDLVILLWQIFDPQRYLETFF 616  
DB 682 ftkiwwhvftkkeeekewrklepwwklyatvgvlgmdvltlaiqgidpplrhtletf 741

QY 617 PLEDPVSTTDDIKIRPELEHCESORNSMWGLVYFGKGLILVFLGLAYETRSIKVQIN 676  
DB 742 akeepkedi-dvslpqlehcscrkmtwlgifyykglllllgliflayecksvstekin 800

QY 677 DSRVYGMISYNNVVLCLITAPVGMVITASQODASFAFVALVIFCCFLSMLLIFYPKVIEW 736  
DB 801 dhravgmalynavclitapvtmilssqdaafafaslaivfssytilvlfvpkmrl 860

QY 737 IRHP--KDKAESYNPDSAISKEDEERYQKLVTEQQLRLITQKEKIRVLRQRLVER 793  
DB 861 itrgevwqseaqdmktgssntnnneeksrllenenrelekieaekeervsvrlrqlqsr 919

RESULT 12  
AAY14101

ID AAY14101 standard; Protein; 961 AA.

XX AAY14101;

XX 21-JUL-1999 (first entry)

XX Human GABAB receptor 1a protein sequence.

XX GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;  
KW transient lower oesophageal sphincter relaxation; spasticity; emesis;  
KW gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;  
KW irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;  
KW autoimmune disease; neoplastic disease; infectious disease; therapy.

XX Homo sapiens.

XX WO9921890-A1.

XX 06-MAY-1999.

XX 27-OCT-1998; 98WO-SE01947.

XX 17-JUL-1998; 98SE-0002575.

XX 27-OCT-1997; 97SE-0003914.

XX 16-MAR-1998; 98SE-0000864.

XX (ASTR ) ASTRA AB.

XX Ekstrand J;

XX WPI; 1999-302985/25.

XX N-PSDB; AAX58054.

XX Polynucleotides encoding human and canine gamma aminobutyric acid

XX Type B receptors, used to screen for compounds that are inhibitors

XX of transient lower oesophageal sphincter relaxations

XX Claim 17; Page 79-84; 222pp; English.

XX This sequence is a human gamma aminobutyric acid type B (GABAB)  
XX receptor of the invention. Nucleic acid molecules encoding GABAB  
XX receptors can be used to screen for compounds that are inhibitors of  
XX transient lower oesophageal sphincter relaxations (TLESR). They can also  
XX be used to screen for agonists or antagonists of the GABAB receptors.  
XX Inhibitors of TLESR are useful for treating gastro-oesophageal reflux  
XX disease. Other uses of GABAB receptors, such as human GABAB R1c or 1d,  
XX comprise diagnosis or treatment of conditions related to GABAB  
XX dysfunction, e.g. epilepsy, psychiatric disorders, emesis, irritable  
XX bowel syndrome, dyspepsia, spasticity, arthritis, allergies, autoimmune  
XX diseases, neoplastic diseases, pain and infectious disease.

XX Sequence 961 AA;

Query Match

Best Local Similarity 46.4%; Score 2030.5; DB 20; Length 961;

Matches 384; Conservative 152; Mismatches 220; Indels 23; Gaps 8;

QY 24 PHLOGGVAGRDPDE--LHIGGIFPIAGKGGWGGOGACMPATRLALDDVKNKPNLLPGFKLI 81

DB 155 phcqvnrtpsherravvigaifpms--ggwpgggacqavemaedvnsrrdlpdyelk 212

QY 82 LHSNDECEPGLGASVYNNLLYNKPKQLMLLAGCTVCTTVAARAKMWNLLIVLCYGASSP 141

DB 213 lihndskcdpgqatkyllyelpndpikilmpgcssvstlvaearmwnllivlysgssp 272

QY 142 ALSDRKRPTLFRTHPSATVHNPTRIKLMKKFGWSRVAILQQAEEVFISTVEDLENRCME 201

DB 273 alsnrqrfptftrhpsatvhnptrvkfkewgwkkiatigttteftstlddleervke 332



```
QY 202 AGVEIVTRQSFLSDPTDAVRNLRRODARIIVGLFYVVAARRVLCEMYKQOYLGRAHWFF 261
DB 333 agieitfrqsfspavpvknkrqdariivglfyetearkvfcevykerlfgkkywvfl 392
QY 262 IGWYEDNWEVNLKAEGITCTVEQMRIRAEGLHTTEALMWNQNTTISGWTAEERHRL 321
DB 393 igwyadnwfk1--ydpstinctvdemteaveghittemlpantrsisnmtsgfvekl 450
QY 322 NOALIEEGYDINHRYPE---GYQEAPLAYDAVMSVALAFNKTMRERLTGKKSRLDFTYT 378
DB 451 tkrl-----krhpeetggfgeaplaydaivalalalnktsgggsgvrledfnyn 501
QY 379 DKEIADEIYAAMNSTQFLGVSQWAFSSQGDRIALTQIEQMDIGRYEKLYGYDTQDLNLS 438
DB 502 ngtitdqiyrarnsssfegvghvfdasgrmawtlieqlggsgykygydstkddls 561
QY 439 WLNTQEWIGGKVPQDRTIVTHVLRVSLPLFCVCMCTISSCGIFVAPALIFINWKNHRRV 498
DB 562 wsktdkwiggspadqtlviktrfksqklfisvslsglglavvclsfniynshvry 621
QY 499 IQSSHPCVNTIMLFGVICILISVILLGIDGRFVSPPEVPKICQARAWLLSTGFTLAYGAM 558
DB 622 iqnsqpnlnltavcslalaavfplgdgyhigrnqpfvcqarlwlglglfsigygs 681
QY 559 FSKVMVRHRTTK--AKTDPKPKVPKLYTMVSGLLSIDLLSWQIFDFPLQRYLETF 616
DB 682 ftkiwwhtvtkkekewrktlepklyatvgilvgmdvltaiwqivdplhrtief 741
QY 617 PLEDPVSTDDIKRPELEHESQRNSMWGLVYGFKGLILVGLFLAYETRSIKVQKIN 676
DB 742 akeepkedi-dvslilpqlehcscrmtwlgifygykglllllglflayetskvsstekin 800
QY 677 DSRVGVMSIYNVVLCLITAPGVNVIASOODASFAFVALAVIFCCFLSMLLIFVPKVIEW 736
DB 801 dhravgmalynavvlclitapvtmllssqdaafafaslaivfssyitvlvlfvpmkrrl 860
QY 737 IRHP--KDKAESKYNPDSAISKEDEERYQKLVTEQQLRITQREKIRVLRQRLVER 793
DB 861 itrgwqseadtmtkgstnnneeksrllekenrelekiiaekeerveiselrhqlqr 919

RESULT 13
AAV49133
ID AAV49133 standard; Protein; 1323 AA.
XX
XX
AC AAV49133;
XX
XX 07-JAN-2000 (first entry)
XX
XX GABA-BRLA*Gqo5 fusion construct protein sequence.
XX
XX G-protein fusion receptor; CaR; calcium receptor; GluR; head injury;
KW metabotropic glutamate receptor; GABABR; chimeric receptor; stroke;
KW gamma-aminobutyric acid receptor; allosteric modulator; antagonist;
KW spinal cord injury; epilepsy; ischaemia; hypoglycaemia; anoxia;
KW Alzheimer's disease; hyperparathyroidism; osteoporosis; depression;
KW cognitive disorder.
XX
OS Homo sapiens.
XX
XX WO9951641-A1.
XX
XX 14-OCT-1999.
PD
XX 02-APR-1999; 99WO-US07333.
XX
XX 03-APR-1998; 98US-0080671.
XX
XX (NPSP-) NPS PHARM INC.
XX
XX Stormann TM, Hammerland LG, Storjohann LL, Busby JG, Garrett JB;
PI Simin RT;
```

```
XX
DR WPI; 1999-610995/52.
XX N-PSDB; AAZ31064.
XX
PT New G-protein fusion receptors and chimeras containing domains from
PT different receptors, used to screen for modulators, potentially useful
PT e.g. for treating or preventing stroke or Alzheimer's disease -
XX
XX
PS Disclosure; Fig 14; 255pp; English.
XX
XX The invention relates to G-protein fusion receptors (I) comprising:
CC (1) in the N to C direction, extracellular (ECD), transmembrane (TMD) and
CC intracellular (ICD) domains, each chosen independently from a CaR
CC (calcium receptor), GluR (metabotropic glutamate receptor) and GABABR
CC (gamma-aminobutyric acid receptor); (2) an optional linker attached to
CC the C-terminus of ICD; and (3) a G-protein (GP) linked to ICD or the
CC linker. (I), and recombinant chimeric receptors (CR) without the GP
CC component, are used to assess function of the various domains and to
CC identify compounds (e.g. allosteric modulators or antagonists) that act
CC on these domains. The modulators are potentially useful for treating or
CC preventing diseases associated with the receptors, e.g. stroke, head or
CC spinal cord injury, epilepsy, ischaemia, hypoglycaemia, anoxia,
CC Alzheimer's disease, hyperparathyroidism, osteoporosis, cognitive
CC disorders and depression. Nucleic acid (II) that encodes (I) is used:
CC (1) for recombinant production of corresponding proteins; and (2) to
CC produce cells used in screening for modulators. Use of CaR and mGluR
CC domains allows presentation of GABABR domains, to a binding agent, in a
CC form more like the natural domain structure compared with use of
CC incomplete receptors, lacking one or more domains. By shuffling different
CC domains, agents can be identified that affect particular domains of a
CC receptor.
XX
XX Sequence 1323 AA;
XX
XX
XX Query Match 46.4%; Score 2030.5; DB 20; Length 1323;
XX Best Local Similarity 49.3%; Pred. No. 4.4e-192;
XX Matches 384; Conservative 152; Mismatches 220; Indels 23; Gaps 8;
XX
QY 24 PHLOGGVAGRPDE--LHIGGIFPIAGKGGHGGQACWPAATRLALDDVKNQPNLLPGFKLI 81
DB 155 phcqvnrphserravyigalfpms--ggwpggqacpavemaledvnrdilpdyelk 212
QY 82 LHSNDECEPGLGASVMYLLNKPQKIMLLAGCSTCTTVAAEAKMNLIVLCYGASSP 141
DB 213 lihhdskdpggqatkyellyndpkiilmpgcsvstlvaaearmnlivisygsssp 272
QY 142 ALSDRKREPTLFRTHPSATVHNTPRIKMKKFGMSRVAILQQAEVEFISTVEDLENRCME 201
DB 273 alsnqrftptfthpsatlhnptrvklfekwgwkkiatigqtevtstlddleervke 332
QY 202 AGVEIVTRQSFLSDPTDAVRNLRRODARIIVGLFYVVAARRVLCEMYKQOYLGRAHWFF 261
DB 333 agieitfrqsfspavpvknkrqdariivglfyetearkvfcevykerlfgkkywvfl 392
QY 262 IGWYEDNWEVNLKAEGITCTVEQMRIRAEGLHTTEALMWNQNTTISGWTAEERHRL 321
DB 393 igwyadnwfk1--ydpstinctvdemteaveghittemlpantrsisnmtsgfvekl 450
QY 322 NOALIEEGYDINHRYPE---GYQEAPLAYDAVMSVALAFNKTMRERLTGKKSRLDFTYT 378
DB 451 tkrl-----krhpeetggfgeaplaydaivalalalnktsgggsgvrledfnyn 501
QY 379 DKEIADEIYAAMNSTQFLGVSQWAFSSQGDRIALTQIEQMDIGRYEKLYGYDTQDLNLS 438
DB 502 ngtitdqiyrarnsssfegvghvfdasgrmawtlieqlggsgykygydstkddls 561
QY 439 WLNTQEWIGGKVPQDRTIVTHVLRVSLPLFCVCMCTISSCGIFVAPALIFINWKNHRRV 498
DB 562 wsktdkwiggspadqtlviktrfksqklfisvslsglglavvclsfniynshvry 621
QY 499 IQSSHPCVNTIMLFGVICILISVILLGIDGRFVSPPEVPKICQARAWLLSTGFTLAYGAM 558
XX
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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 19, 2002, 10:51:08 ; Search time 19 Seconds  
(without alignments)  
1300.803 Million cell updates/sec

Title: US-09-715-962-2

Perfect score: 4374

Sequence: 1 MRKDMTSDGAVTFWIFLLCL.....LINSSAHATPAATLAITQGE 840

Scoring table: BLOSUM62.

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Issued\_Patents\_AA.\*

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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/PCrUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	2035	46.5	844	4	US-09-422-936-51
2	2034.5	46.5	899	4	US-09-422-936-71
3	2032	46.5	844	4	US-09-422-936-47
4	2031.5	46.4	964	4	US-09-422-936-53
5	2030.5	46.4	961	4	US-09-422-936-49
6	2029.5	46.4	892	4	US-09-422-936-75
7	2029.5	46.4	960	4	US-09-422-936-45
8	1967	45.0	886	4	US-09-422-936-77
9	1209.5	27.7	461	4	US-09-422-936-57
10	1206	27.6	581	4	US-09-422-936-59
11	1205	27.5	578	4	US-09-422-936-55
12	1158.5	26.5	859	3	US-09-183-253-2
13	1072.5	24.5	496	4	US-09-422-936-85
14	1033	23.6	563	4	US-09-422-936-79
15	697.5	15.9	332	3	US-09-183-253-4
16	359	8.2	908	4	US-08-855-146-2
17	355.5	8.1	908	3	US-08-823-110-1
18	355.5	8.1	908	3	US-08-604-298-1
19	355	8.1	915	4	US-08-617-785-12
20	355	8.1	922	4	US-08-617-785-14
21	353	8.1	912	4	US-08-617-785-2
22	353	8.1	912	4	US-09-641-318-2
23	353	8.1	915	1	US-08-453-862-2
24	353	8.1	915	2	US-08-452-734A-2
25	353	8.1	915	4	US-08-176-401B-2
26	353	8.1	915	5	PCT-US94-14989-2
27	349.5	8.0	912	5	PCT-US91-09422-19

28	328	7.5	879	1	US-08-072-574-6	Sequence 6, Appli
29	328	7.5	879	1	US-08-486-270-6	Sequence 6, Appli
30	328	7.5	879	3	US-08-367-264-6	Sequence 6, Appli
31	328	7.5	879	4	US-09-153-757-6	Sequence 2, Appli
32	327	7.5	872	3	US-08-337-797A-2	Sequence 2, Appli
33	327	7.5	872	3	US-09-258-523-2	Sequence 2, Appli
34	323	7.4	879	4	US-08-794-158-2	Sequence 2, Appli
35	321.5	7.4	867	4	US-08-617-785-4	Sequence 2, Appli
36	313.5	7.2	877	2	US-08-407-875-2	Sequence 2, Appli
37	313.5	7.2	877	4	US-09-277-858-2	Sequence 2, Appli
38	311.5	7.1	877	3	US-09-126-280-2	Sequence 2, Appli
39	302.5	6.9	1180	4	US-08-660-148-2	Sequence 2, Appli
40	297.5	6.8	1212	4	US-08-660-148-5	Sequence 5, Appli
41	283.5	6.5	1180	1	US-08-486-270-8	Sequence 8, Appli
42	283.5	6.5	1180	3	US-08-367-264-8	Sequence 8, Appli
43	283.5	6.5	1180	4	US-09-153-757-8	Sequence 8, Appli
44	282.5	6.5	1180	1	US-08-072-574-8	Sequence 8, Appli
45	281	6.4	856	4	US-09-619-353-8	Sequence 8, Appli

## ALIGNMENTS

RESULT 1

US-09-422-936-51

; Sequence 51, Application US/09422936

; Patent No. 6465213

; GENERAL INFORMATION:

; APPLICANT: Ekstrand, Jonas

; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES

; FILE REFERENCE: 06275-165002

; CURRENT APPLICATION NUMBER: US/09/422,936

; CURRENT FILING DATE: 1999-10-22

; PRIOR APPLICATION NUMBER: US 09/242,608

; PRIOR FILING DATE: 1999-02-19

; PRIOR APPLICATION NUMBER: PCT/SE98/01947

; PRIOR FILING DATE: 1998-10-27

; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2

; PRIOR FILING DATE: 1997-10-27

; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2

; PRIOR FILING DATE: 1998-03-16

; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2

; PRIOR FILING DATE: 1998-07-17

; NUMBER OF SEQ ID NOS: 85

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 51

; LENGTH: 844

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-422-936-51

Query Match

Best Local Similarity 46.5%; Score 2035; DB 4; Length 844;

Matches 387; Conservative 151; Mismatches 219; Indels 28; Gaps 9;

QY	23	SPHL---QGVAGRPDE---LHIGGIPTAGGGGQACMPATFALDDVKNPPLL	75
DB	32	SPHLPRHSRVPHPSPERRAVYIGALFPM--GGPPGQACQPAVEMALDVSRRDIL	89
QY	76	PGFKLIHNSDCEPGLGASVMYLNKPKQLMLIAGCTVCTTVAEAAKMWNLIVLC	135
DB	90	PDYELKLIHDSKCDGQATKYLYELLYNDPKIILMPGSSYSTLVAAARWNLIVLS	149
QY	136	YGASSPALSDRRPPTLFRTHPSATVHNPTRIKLMKFGWSRVAILQQAEEVISTVEDL	195
DB	150	YGSSSPALSNRQRPFFRTHPSATLHNPTRVKLFKGGWKKIATIQTTFTVSTLDDL	209
QY	196	ENRCMEAGVEIVTRQSFSDPTDAVRLRRQDARIIVGLFYVVAARRVLCENTKQOYLGR	255
DB	210	EERVKEAGIEITPROSFSDPAVPVKNLKRQDARIIVGLFYETEARVFCVYKERLFGK	269
QY	256	AHWFFIAGVNDWYEVNLKAEGITCTVQMRTAAGHLTTEALMNQNNQTTISGMTAE	315



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; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-422-936-47

Query Match          46.5%; Score 2032; DB 4; Length 844;
Best Local Similarity 49.1%; Pred. No. 7e-198;
Matches 388; Conservative 151; Mismatches 213; Indels 38; Gaps 9;

QY 23 SPHLOGGAGRPD-----ELHIGGIFPIAGKGGWGGQACMPATRLALDDVKNK 70
DB 32 SPHLP-----RPHRPVPHSPERRAVYIGALFPMs--GGWPGGACQPAVEMALDVNS 84
QY 71 QPNLLPGFKLLIHSNDSCEPGLGASVMYLLYKPKMLLAGSTVCTTVAEAAKMN 130
DB 85 RRDLPDYELKLIHSDKCDQATKYLYELLYNDPIKIILMPGSSVSTLVAEAAKMN 144
QY 131 LIVLCYGASSPALSDRKRPFTLFRPHSATVHNPTRIKLMKFGWSRVAILQOAEVETS 190
DB 145 LIVLSGSSPALSNRQRPFTFRPHSATLHNPTRVKLFERKGNKTIATIOQTTEVETS 204
QY 191 TVEDLENRCEAGVEIVTRQSFSDPTDAVRLNRQDARIIVGLFYVAARVLCEMYKQ 250
DB 205 TLDDLEERVKEAGIEITFRQSFSDPAVPVKNLQDARIIVGLFYETEARKVCEVYKE 264
QY 251 QLYGRAHVWPIGWEDNMYEVNKAEGITCTVEQMRTAAEGHLTEALMNNQNTTIS 310
DB 265 RLFGKYYWFLIGYADNWFKT--YDPSINCTVDEMTAEVGHITTEIVMLNPANTRTS 322
QY 311 GMTAEERHRLNQALIEBGYDINHRYPE---GYQEAFLAYDAVMSVALAFNKTWERLTT 367
DB 323 NMTSQEFVEKLTURL-----KRHPETGGFQEAFLAYDAIHALALANKTSGGGGR 373
QY 368 GKSLRDTFYDKEADEIYAAMNSTQFLGVSGVAVFSSQGDRIALTQEQMIDGKYEKL 427
DB 374 SGVLEDFENYNNQITDQIYRAMNSSSEFEGVGHVVDASGRMAWTLEQLGGYSKKI 433
QY 428 GYDTQDLDNLISWLNTEQWIGKVPQDRTIVTHVLTVSLPLFVCMCTISSCGIFVAFALI 487
DB 434 GYDSTKDDLWSKTDKWIIGSPADQTLVKTFRFLSQKLFISVLSLGLVLAUVCL 493
QY 488 IFNTWKNHRRVIOSSHPCVNTIMLFVLIICLISVILLGIDGRFVSPEEPKICQARWLL 547
DB 494 SFNLYSHRVYIQSNQNLNLTAVGCSLAAAVFPLGLDGYHIGRSQFPFVCQARWLL 553
QY 548 STGFTLAYGAMFSKVRVHRETTK--AKTDPKKVPEPKLYTMVSGLLSIDLVILLSWOI 605
DB 554 GLGSLGYSNFTKIWWVHTVFTKEEKEKWKRLTEPKLYTAVGLLVGMVDVLTALWQI 613
QY 606 FDPQRYLETFLPDDVSTTDIKIRPELEHCESQNSMMLGLVYGFKGLILVFLGLAY 665
DB 614 VDPHRTIETFAKEEKREDI-DVSLPQLEHCSSKKMNTWLGIFGYKGLLLGLIFLAY 672
QY 666 ETRSIKVKQINDSRVYMSIYNNVVLCLITAPGVHVIASQDASFAFVALAVIFCCFLSM 725
DB 673 ETKSVSTEKLNDRHRAVGMAIYNNVAVLCITAPVTMILSSQDAAAFASLAIVFSSYTL 732
QY 726 LLIFVPKVIEWIRHPKDAESK--YNPDSATSKDEERYQKLVTENEOLRLITQKEKI 783
DB 733 VVLFVPKMRRLITRGESQETQDTMKTGSGSTNNNEEKSRLLEKENRELEKIIAEKERV 792
QY 784 RVLQRQLVR 793
DB 793 SELRHQLQSR 802

RESULT 4
US-09-422-936-53
```

```
; Sequence 53, Application US/09422936
; Patent No. 6465213
; GENERAL INFORMATION:
; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/09/422,936
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 09/242,608
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-422-936-53

Query Match          46.4%; Score 2031.5; DB 4; Length 964;
Best Local Similarity 49.4%; Pred. No. 1e-197;
Matches 386; Conservative 152; Mismatches 216; Indels 27; Gaps 9;

QY 24 PHLOGGAGRPD-----LHIGGIFPIAGKGGWGGQACMPATRLALDDVKNQPNLLPGFK 79
DB 158 PHCQ--VSRPHSERRAVYIGALFPMs--GGWPGGACQPAVEMALDVNSRRDILPDYE 213
QY 80 LLIHSNDSCEPGLGASVMYLLYKPKMLLAGSTVCTTVAEAAKMNLIIVLCYGAS 139
DB 214 LKLIHSDKCDQATKYLYELLYNDPIKIILMPGSSVSTLVAEAAKMNLIIVLSYGS 273
QY 140 SPALSDRKRPFTLFRPHSATVHNPTRIKLMKFGWSRVAILQOAEVETSTVEDLENRC 199
DB 274 SPALSNRQRPFTFRPHSATLHNPTRVKLFERKGNKTIATIOQTTEVFTSTUDDLEERV 333
QY 200 MEAGVEIVTRQSFSDPTDAVRLNRQDARIIVGLFYVAARVLCEMYKQLYGRAHVW 259
DB 334 KEAGIEITFRQSFSDPAVPVKNLQDARIIVGLFYETEARKVCEVYKERLFGKYYW 393
QY 260 FIGWTEDNMYEVNKAEGITCTVEQMRTAAEGHLTEALMNNQNTTISGMTAEERH 319
DB 394 FLIGWYADNWFKT--YDPSINCTVDEMTAEVGHITTEIVMLNPANTRTSINMTSQEFVE 451
QY 320 RLNQALIEBGYDINHRYPE---GYQEAFLAYDAVMSVALAFNKTWERLTTGKKSRLDFT 376
DB 452 KTKRL-----KRHPETGGFQEAFLAYDAIHALALANKTSGGSRGSRVRLDFN 502
QY 377 YTDKEIADYEIYAAMNSTQFLGVSGVAVFSSQGDRIALTQEQMIDGKYEKLGYDQDNL 436
DB 503 YNNQITDQIYRAMNSSSEFEGVGHVVDASGRMAWTLEQLGGYSKKIYGYDSTKDD 562
QY 437 LSWLNTEQWIGKVPQDRTIVTHVLTVSLPLFVCMCTISSCGIFVAFALIINWKNHR 496
DB 563 LSWSKTDKWIIGSPADQTLVKTFRFLSQKLFISVLSLGLVLAUVCLSFNIYNSHV 622
QY 497 RVIOSSHPCVNTIMLFVLIICLISVILLGIDGRFVSPEEPKICQARWLLSGFTLAYG 556
DB 623 RYIQNSQPNLNLITAVGCSLAAAVFPLGLDGYHIGRSQFPFVCQARWLLGLGSLGY 682
QY 557 AMFSKVRVHRETTK--AKTDPKKVPEPKLYTMVSGLLSIDLVILLSWOIFDPLQRYLE 614
DB 683 SMFTKIWWVHTVFTKEEKEKWKRLTEPKLYTAVGLLVGMVDVLTALWQVDPDLHRTIE 742
QY 615 TFPLEDPVSTTDIKIRPELEHCESQNSMMLGLVYGFKGLILVFLGLAYETRSIKVKQ 674
DB 743 TFAKEEKREDI-DVSLPQLEHCSSKKMNTWLGIFGYKGLLLGLIFLAYETKSVSTEK 801
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; LENGTH: 886
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-422-936-77

Query Match          45.0%; Score 1967; DB 4; Length 886;
Best Local Similarity 48.0%; Pred. No. 3.3e-191;
Matches 375; Conservative 152; Mismatches 215; Indels 40; Gaps 8;

Qy 19 CLTASPHLGGVAGRDELHIGGIFPIAGKGGWGGQACMPATRLALDDVKNKPNLLPGF 78
Db 96 CVNRTPHSERRA-----VIGALF-----PAMEALEDVNSRRDILPDY 134
Qy 79 KILHNSDSECEPGLGASVYNNLYNKPQKMLLAGCSTVCTTVAEAAKMNLIYCYGA 138
Db 135 ELKLIHDSKCDPGQATKYLYELLYNDPIKIILMPGCSVSTLVAEAAKMNLIYSGS 194
Qy 139 SPALSDRRKRPFTLFRTHPSATVHNTPRIKMKKFGWSRVAILQOAEVFIISTVEDLNR 198
Db 195 SSPALSNRRQFTFFRTHPSATLHNTPRVKLFKFGWKWKIATIQOTTEVFTSLDLEER 254
Qy 199 CMEAGVEIVTROSFLSDPTDAVNLRARQDARIIVGLFYVVAARRVLCMKQOOLYGRAHV 258
Db 255 VKEAGIEITFRGSFSDPAVPVKNLRQDARIIVGLFYETEARKVCEVTKERLFGKYV 314
Qy 259 WFFIGMYEDNWEVNLKAEGITCTVEQMRIAEGHLITTEALMNNQNTTISGMTAEFR 318
Db 315 WFLIGYADNWFKI--YDPSINCTVDEMTAEVGHITTEIVMLNPANTRISNMTSQEFV 372
Qy 319 HRLNQALIEEGVDINHRYPE---GYOEAPLAYDAVMSVALAFNKNMERLTTGKKSURDF 375
Db 373 EKLTREL-----KRHPETGGFQEAPLAYDAIWAALALNKITQOTTEVFTSLDLEER 423
Qy 376 TYTDKEIADEIYAAMNSTOFLGVSQVAFSSQGDRIALTOIEOMIDKYEKLGYDFTOLD 435
Db 424 NYNNQITQIYRAMNSSSFEVSGHVVFDASGRMAWTLIEQLGGSYKKGIDYSTKD 483
Qy 436 NLSWLNTEQWIGKVPQDRTIVTHVLRVSLPLFVCMCTISSGIFVAFALIIFNKNH 495
Db 484 DLSWKTDRWIGSPPADQTLVTKTRFLSQKLFISVSVLSLGLVAVCLSFNINSH 543
Qy 496 RVIQSHVPCNTIMLFGVILICILSVILIGIDGRFVSPPEYKICQARALLSTGFTLAY 555
Db 544 VRYIQNSQPNLNLTAVGCSLAAVAPFLGLDGYHGRNQFPFVQCARLLGLGFGSLGY 603
Qy 556 GAFSKVWVRHRETTK--AKTDPKKKVEPKVLYTMVSGLLSIDLVILLSHQIDPLQRYL 613
Db 604 GSNFTKIWWVHTVFTTKKEKWKRLTEPKVLYATVGLLVGMDVLTIAIWOIVDPLHRTI 663
Qy 614 ETPFLEDPVSTTDDIKRIPLECHESORNSMWLGLVYFKGLILVFLGLAYETRSIKVK 673
Db 664 ETFAKEEPKEDI-DVSIPLPOLEHSCSRKMTWLGIFYGKGLLLGIFLAYETKSYSTE 722
Qy 674 QINDSYGMSYNNVVVLCILITAPVGMVIAQQDASFAFVALAVIFCCFLSMLLIFVPKV 733
Db 723 KINDHRAVGMAIYNVAVLCILITAPVTMILSSQQDAFAFASLAIVFSSYITLVVLFVPM 782
Qy 734 IEVIRHP--KDKAESYNPDSAISKEDERYOKLVITENEOLQRLITOKEKIRVLRORLV 791
Db 783 RRLITRGEOAQDQWTKTGSSTNNNEEKSRLLEKENRELEKIIAEKEERSVSELHQ 842
Qy 792 ER 793
Db 843 SR 844

RESULT 9
US-09-422-936-59
; Sequence 59, Application US/09422936
; Patent No. 6465213
; GENERAL INFORMATION:
; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/09/422.936
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 09/242,608
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2
```



; PRIOR FILING DATE: 1997-10-27  
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2  
; PRIOR FILING DATE: 1998-03-16  
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2  
; PRIOR FILING DATE: 1998-07-17  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 59  
; LENGTH: 581  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-09-422-936-59

Query Match 27.6%; Score 1206; DB 4; Length 581;  
Best Local Similarity 53.5%; Pred. No. 7.4e-114;  
Matches 230; Conservative 73; Mismatches 105; Indels 22; Gaps 6;

QY 24 PHLOGGVAGRPDE---LHIGGIFPIAGKGGWGGGACMPATRLALDDVKNQPNLLPGPK 79  
Db 158 PHCQ--VSRTPHSERRAVYIGALFFMS--GGWPGGACQAPVEMALEDVNSRRDILPDYE 213  
QY 80 LILHSDSECEPGLGASVMYNNLYNKPQKMLLAGCSTVCTTVAEAAKMNLIIVLCYGAS 139  
Db 214 LKLHSDSKDPGQATKYLYELLYNDPIKILMPGSCSSVSTLVAEARMNLIIVLSYGS 273  
QY 140 SPALSDRKRFPFLFTHPSATVHNTRIKLKKFGWSRVAILQQAEEVFISTVEDLENRC 199  
Db 274 SPALSNRQRFPTFFTHPSATLHNTRVKLFKKGWKRIATIQOTTEVFTSLDLEERV 333  
QY 200 MEAGVEIVTROSFSDPDAVNRRLRQDARIIVGLFYVVAARRVLCEMYKQOLYGRAHVW 259  
Db 334 KEAGIEITFRQSFSDPAPVKNLRQDARIIVGLFYETEARVCEVYKERLFGKKYVW 393  
QY 260 FFIGWEDNWTVEVNLKAGICTVQMRIAARGHLTTTEALMNNQNTTISGMTAEFRHL 319  
Db 394 FLIGWADNWEKT--YDPSINCTVDETEAVEGHITTEIVMLNPANTRISNMTSOEFVE 451  
QY 320 RLNQALIEEGYDINHRYPE---GYOEAPLAYDAVMSVALAFNKMTWRLTTGKKSLRDP 376  
Db 452 KLTKRL-----KRHEETGGFQEAPLAYDAIWAALALANKTSGGSGRSGVRLEDN 502  
QY 377 YDKEIADEIYAAMNSTOFLVSGVVAFFSSQGDRIALQIEQMDGKYEKLGYYDTQLDN 436  
Db 503 YNNQITDQIYRAMNSSFEGVSHVFDASGRMAWTLIEQLGGSYKKIGYDSTKDD 562  
QY 437 LSWLNTQWI 446  
Db 563 LWSKTDKWI 572

RESULT 11  
US-09-422-936-55  
; Sequence 55, Application US/09422936  
; Patent No. 6465213  
; GENERAL INFORMATION:  
; APPLICANT: Ekstrand, Jonas  
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES  
; FILE REFERENCE: 06275-165002  
; CURRENT APPLICATION NUMBER: US/09/422,936  
; CURRENT FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: US 09/242,608  
; PRIOR FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: PCT/SE98/01947  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2  
; PRIOR FILING DATE: 1997-10-27  
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2  
; PRIOR FILING DATE: 1998-03-16  
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2  
; PRIOR FILING DATE: 1998-07-17  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 55

; LENGTH: 578  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-422-936-55

Query Match 27.5%; Score 1205; DB 4; Length 578;  
Best Local Similarity 53.3%; Pred. No. 9.3e-114;  
Matches 228; Conservative 74; Mismatches 108; Indels 18; Gaps 5;

QY 24 PHLOGGVAGRPDE--LHIGGIFPIAGKGGWGGGACMPATRLALDDVKNQPNLLPGFKLI 81  
Db 155 PHCQVNRTPHSERRAVYIGALFFMS--GGWPGGACQAPVEMALEDVNSRDILPDYELK 212  
QY 82 LHSNDECEPGLGASVMYNNLYNKPQKMLLAGCSTVCTTVAEAAKMNLIIVLCYGASSP 141  
Db 213 LIHSDSKDPGQATKYLYELLYNDPIKILMPGSCSSVSTLVAEARMNLIIVLSYSSSP 272  
QY 142 ALSDRKRFPFLFTHPSATVHNTRIKLKKFGWSRVAILQQAEEVFISTVEDLENRCME 201  
Db 273 ALSNRQRFPTFFTHPSATLHNTRVKLFKKGWKRIATIQOTTEVFTSLDLEERVKE 332  
QY 202 AGVEIVTROSFSDPDAVNRRLRQDARIIVGLFYVVAARRVLCEMYKQOLYGRAHVWF 261  
Db 333 AGIEITFRQSFSDPAPVKNLRQDARIIVGLFYETEARVCEVYKERLFGKKYVWFL 392  
QY 262 IGWEDNWTVEVNLKAGICTVQMRIAARGHLTTTEALMNNQNTTISGMTAEFRHL 321  
Db 393 IGWADNWEKI--YDPSINCTVDETEAVEGHITTEIVMLNPANTRISNMTSOEFVEKL 450  
QY 322 NQALIEEGYDINHRYPE---GYOEAPLAYDAVMSVALAFNKMTWRLTTGKKSLRDP 378  
Db 451 TKRL-----KRHEETGGFQEAPLAYDAIWAALALANKTSGGSGRSGVRLEDN 501  
QY 379 DREIADEIYAAMNSTOFLVSGVVAFFSSQGDRIALQIEQMDGKYEKLGYYDTQLDNLS 438  
Db 502 NOTITDQIYRAMNSSFEGVSHVFDASGRMAWTLIEQLGGSYKKIGYDSTKDDLS 561  
QY 439 WLNTQWI 446  
Db 562 WSKTDKWI 569

RESULT 12  
US-09-183-253-2  
; Sequence 2, Application US/09183253  
; Patent No. 6043054  
; GENERAL INFORMATION:  
; APPLICANT: VAWTER, LISA  
; APPLICANT: STAMMERS, MELANIE  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Ratner & Prestia  
; STREET: P.O. Box 980  
; CITY: Valley Forge  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/183,253  
; FILING DATE: 30-OCT-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 9817907.0  
; FILING DATE: 17-AUG-1998  
; APPLICATION NUMBER: 60/075,306  
; FILING DATE: 20-FEB-1998  
; ATTORNEY/AGENT INFORMATION:



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Db 482 KTDKWI 487
|::||
RESULT 14
US-09-422-936-79
; Sequence 79, Application US/09422936
; Patent No. 6465213
; GENERAL INFORMATION:
; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/09/422.936
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 09/242,608
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 563
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-422-936-79

Query Match 23.6%; Score 1033; DB 4; Length 563;
Best Local Similarity 41.8%; Pred. No. 3, 2e-96;
Matches 207; Conservative 101; Mismatches 157; Indels 30; Gaps 6;

QY 328 EGYDINHRYPEGYQAEPLAYDAVMSV-ALAFNKTMERLTG-----KKSLRDFTY 377
Db 28 EGCGIIHPWPBGIRYGLTRDQKAINFLPVDYEVYVCRGEREVGVKVRKCLANGSW 87
QY 378 TDKE-----IADEIYAAMNSTQFLGVGVAFSSQGDRIALTOIEQMDG 422
Db 88 TDMTPSRCAVICSYSYLTITDQIYRAMNSSFEVGVVDFDASGRMAWTLIEQLQGG 147
QY 423 KYEKLGYDTOLDNLWLNTBQWIGGKVPQDRTIVTHVLTSLPLFVCMCTISSCGIFV 482
Db 148 SYKKGIDYDSTKDLSSKTDKWKGGSPADQTLVIKTRFLSKQLFISVSLSLGIVL 207
QY 483 AFALIFNIWKKRRVYQSSHPVCNTIMLFGVVICLSVILLGIDGRFVSPPEYKICQA 542
Db 208 AVVCLSENIYNSHVRYIONSQPNLNLTAVCSLALAAVPLGLDGYHIGRNOFPFVCOA 267
QY 543 RAWLLSTGFTLAYGAMSKVWRVHRFTTK--AKTDPKKKVPWKLYTVMVSGLLSIDLVIL 600
Db 268 RLWLLGLGFLSLGYSMETKIMWHTVFTKKEKKEWRTLEPWKLYATVGLLVGMDVLT 327
QY 601 LSWQIEDPLORYLETFFLEDVSTDDIKIRPELEHCSQRNSMWLGLVYGFKGLLIVFG 660
Db 328 AIVQIVPLHRTIETFAKEEPKEDI-DVSILPQLEHCSRRKMTWLGIFYGKGLLLLG 386
QY 661 LFLAYETRSIKVKOINDSRVYGMISYNNVVLCLITAPVGMVIASOODAFVALAVIFC 720
Db 387 IFLAYETKSVSTEKINDHRAVGMAYVAVLCLITAPVTMILSSOODAFAFASIAVFS 446
QY 721 CFLSMLLIFVPKVIETVIRHP--KDKAESKNPDSAISKEDPEYOKLVTEQLOQLITQ 778
Db 447 SYTLVVLVFPKMRRLITRGWEQSEADTMKTGSSNTNNNEEKSLLEKENRELEKIAT 506
QY 779 KEERKIRVLQRLVER 793
Db 507 KEERSVELRQLOQR 521
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RESULT 15
US-09-183-253-4
; Sequence 4, Application US/09183253
; Patent No. 6043054
; GENERAL INFORMATION:
; APPLICANT: VAWTER, LISA
; APPLICANT: STAMMERS, MELANIE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/183,253
; FILING DATE: 30-OCT-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9817907.0
; FILING DATE: 17-AUG-1998
; APPLICATION NUMBER: 60/075,306
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70395
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-183-253-4

Query Match 15.9%; Score 697.5; DB 3; Length 332;
Best Local Similarity 41.4%; Pred. No. 2, 2e-62;
Matches 135; Conservative 74; Mismatches 110; Indels 7; Gaps 6;

QY 372 LRDFYTDKEIADEIYAAMNSTQFLGVGVAFSSQGDRIALTOIEQMDGKYKLGYYD 431
Db 2 IQDFNYTDHTRILNANMETNFFGVTVGVVFRN-GERMGITIKFTQFQDSREVKVGEYN 60
QY 432 TOLDNLWLNL-TEQWIGGKVPQDRTIVTHVLTSLPLFVCMCTISSCGIFVAFALIFN 490
Db 61 AVADTLEIINDTRIQGSEPPKDKTILIEQLRKISLPLYSILSALTILGIMIMASAFLEFN 120
QY 491 IWNKRRVYQSSHPVCNTIMLFGVVICLSVILLGIDGRFVSPPEYKICQARAWLLSTG 550
Db 121 IKNRQKLIKMSPPYNNNLILGGLMSYASIFLGLDGSFVSEKTEETLCTVTRWLTIVG 180
QY 551 FTLAYGAMSKVWRVHRFTTKAKTDPKKVPEWKLYTVMVSGLLSIDLVILLSQIFDPLQ 610
Db 181 YTTAFGAMFAKTRVHAIFKNVKM-KKKIKQKLLIVGGMLLIDLCILICWQAVDPLR 239
QY 611 RYLETFPLE-DPVSTDDIKIRPELEHCSQRNSMWLGLVYGFKGLLIVGLFLAYETRS 669
Db 240 RTVEKYSMEPDAGR--DISIRPLEHCENTHMTIWLGIYAYKGLLMLFGFLAWETRN 297
QY 670 IKVKOINDSRVYGMISYNNV-VVLCIL 694
|::||
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Db 298 VSIPALNDSKYIGMSVYNVGIISCR1 323

Search completed: November 19, 2002, 10:51:40  
Job time : 24 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2002, 10:51:09 ; Search time 11 Seconds  
(without alignments)  
1195.969 Million cell updates/sec

Title: US-09-715-962-2  
Perfect score: 4374  
Sequence: 1 MRKDWTSBGAVTWIFLLCL.....LINSSAHATPAATLAITQGE 840

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues  
Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications\_AA:\*
- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep.\*
  - 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep.\*
  - 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep.\*
  - 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB pep.\*
  - 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep.\*
  - 6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB pep.\*
  - 7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB pep.\*
  - 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB pep.\*
  - 9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB pep.\*
  - 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB pep.\*
  - 11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep.\*
  - 12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB pep.\*
  - 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*
  - 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	2035	46.5	844	10	US-09-875-724-8
2	2032	46.5	844	9	US-09-793-139-55
3	2032	46.5	844	10	US-09-818-879-55
4	2032	46.5	844	10	US-09-211-755B-55
5	2032	46.5	844	10	US-09-875-724-6
6	2030.5	46.4	960	10	US-09-826-508-14
7	2029.5	46.4	793	10	US-09-875-724-4
8	2029.5	46.4	960	10	US-09-211-755B-56
9	2029.5	46.4	960	10	US-09-875-724-2
10	1290	29.5	941	9	US-09-793-139-47
11	1290	29.5	941	10	US-09-818-879-47
12	1290	29.5	941	10	US-09-211-755B-47
13	1284	29.4	898	9	US-09-793-139-2
14	1284	29.4	898	10	US-09-818-879-2
15	1284	29.4	898	10	US-09-211-755B-2
16	1283	29.3	940	10	US-09-818-879-4
17	1283	29.3	940	10	US-09-211-755B-4
18	1248.5	28.5	929	9	US-09-793-139-4
19	1158.5	26.5	874	10	US-09-826-508-26

20	697.5	15.9	332	10	US-09-826-508-28	Sequence 28, Appli
21	355	8.1	915	10	US-09-817-464-12	Sequence 12, Appli
22	355	8.1	922	10	US-09-817-464-14	Sequence 14, Appli
23	353	8.1	912	10	US-09-817-464-2	Sequence 2, Appli
24	321.5	7.4	867	10	US-09-817-464-4	Sequence 4, Appli
25	305	7.0	1203	12	US-10-027-923-5	Sequence 5, Appli
26	297.5	6.8	1212	12	US-10-027-923-4	Sequence 4, Appli
27	232.5	5.3	828	10	US-09-816-685-4	Sequence 4, Appli
28	227	5.2	1078	10	US-09-727-205-2	Sequence 2, Appli
29	219.5	5.0	1078	12	US-10-002-854-2	Sequence 2, Appli
30	205	4.7	839	9	US-09-897-427A-4	Sequence 4, Appli
31	199	4.5	843	12	US-10-124-598-2	Sequence 2, Appli
32	195	4.5	843	12	US-10-124-598-1	Sequence 1, Appli
33	194.5	4.4	852	10	US-09-796-338A-14	Sequence 14, Appli
34	192.5	4.4	604	10	US-09-820-809-13	Sequence 13, Appli
35	190.5	4.4	852	9	US-09-897-427A-6	Sequence 6, Appli
36	184	4.2	841	10	US-09-819-946-2	Sequence 2, Appli
37	180	4.1	841	9	US-09-897-427A-2	Sequence 2, Appli
38	178.5	4.1	763	10	US-09-819-946-4	Sequence 4, Appli
39	175	4.0	481	10	US-09-817-464-8	Sequence 8, Appli
40	172	3.9	926	10	US-09-816-685-2	Sequence 2, Appli
41	167.5	3.8	881	10	US-09-982-736-2	Sequence 2, Appli
42	166	3.8	669	12	US-10-124-598-7	Sequence 7, Appli
43	164	3.7	927	12	US-10-003-356-8	Sequence 8, Appli
44	162.5	3.7	464	10	US-09-796-338A-25	Sequence 25, Appli
45	162	3.7	1215	10	US-09-775-181-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-09-875-724-8  
; Sequence 8, Application US/09875724  
; Patent No. US20020091250A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaupmann, Klemens  
; APPLICANT: Bettler, Bernhard  
; APPLICANT: Bittiger, Helmut  
; APPLICANT: Frost, Wolfgang  
; APPLICANT: Mickel, Stuart J  
; TITLE OF INVENTION: Metabotropic GABA[B] Receptors, Receptor-specific  
; TITLE OF INVENTION: Ligands and their uses  
; FILE REFERENCE: 4-20876/A/PCT  
; CURRENT APPLICATION NUMBER: US/09/875,724  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/194,382  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-25  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 844  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-875-724-8

Query Match	46.5%	Score	2035;	DB 10;	Length	844;	
Best Local Similarity	49.3%	Pred. No.	4e-172;				
Matches	387;	Conservative	151;	Mismatches	219;	Gaps	28;
QY	23	SPHL--OQGVAGRDPDE---	LHIGGIFPIAGKGWGGGACMPATRLALDDVNKPOLL	75			
Db	32	SPHLPRHRSVPHPSSERRAVTIGALFPMS--	CGWPGGACQAPVEMAEADVNSRRDIL	89			
QY	76	PGFKLILHNSDCEPGLGASVYNNLLYKPKMLLAGCSTVCTTVAEAAKMNLIVLC	135				
Db	90	PDYELKLIHDSKDCPDQATKYLYELLYNDPIKILMPGSSVSTLVAEARMNLIVLS	149				
QY	136	YGASSPALSDRKRPPTLFTRHPSPATVHNPTRIKLMKFKGWSRVAILQQAEEVFISTVEDL	195				
Db	150	YGSSSPALSNRQRPPTFFRTHPSATLHNPTRVKLFKWKWKTIATIQQTTEVFTSLDDL	209				
QY	196	ENRCMEAGVEIVTRQSFSDPTDAVRNLRRQARIIVGLFYVVAARRVLCENYKQOYLGR	255				

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Db 210 EERKEAGIEITFROSFFSDPAPVKNLRODARIIVGLFYETEARKEVCEVYKERLFGK 269
QY 256 AHWFIEGWNEDWYEVNLEKAGIEITCIVQMRITAEAGHLITTEALMNNQNTTISGTAE 315
Db 270 KYVWFLIGWADNWKFI--YDPSINCTVDEMTAEVGHITTEIVMLNPANTRISNNTSQ 327
QY 316 EFRHLNQAALIEEGYDINHRYPE---GYQEPALAYDAVWSVALAANKTKMERLITTKKSL 372
Db 328 EVEKLTIKRL-----KRHPEETGGFQEPALAYDAIWAALALANKTSGGGRGVRL 378
QY 373 RQFTYTDKIEADEIYAAMSTOFLGSGVVAFFSSOGDRIALTOIEOMIDGKYELGYDT 432
Db 379 EDENYNNQITDOIYRAMSSSEFGVGHVFDASGRNWTILIEOLOGGYSYKKGIDYS 438
QY 433 QLDNLISWLNTEOWIGKVPQDRTIVPHVLTIVSLPLFVCMCTISSCGIFVAFALIIFNW 492
Db 439 TKDDLWSKTDKWIGSPPADQTLVTKTFRFLSOKLFISVSVLSLGLVAVCLSENIY 498
QY 493 NKHRRVIOSSHVPVCNTIMLFGVILICISVILLGIDGRFVSPPEYKICQARAWLLSTGFT 552
Db 499 NSHVRYIQNSQPNLNLTAAGCSLAAVFPPLGIDGYHIGRNQFPFVCOARLWLLGLGFS 558
QY 553 LAYGAMFSKVRVHRETTK--AKTDPKKKVPEPKLYTMVSGLLSIDLVILLSQIDPLQ 610
Db 559 LGYGSMTKIWWVHTTKKEKKEKWKTLPEPKLYATVGLLVGMDVLTALWQIVDPLH 618
QY 611 RYLETFPLEDPVSTDDIKIRPELEHESORNSMWLGLVYGFGLIIVFLGFLAYETRSI 670
Db 619 RTIETFAKEEPREDI--DVSILPOLEHCSRKMTWLGIYGYKGLLLGIFLAYETKSV 677
QY 671 KYKQINDSRVYGMISYVNVVLCITAPVGMVIAASQODASFVAFVALAIFCCFLMLIFV 730
Db 678 STEKINDHRAVGMAYINVAVLCITAPVTMILSSQODAAFAFASLAIVFSSYITLVVLFV 737
QY 731 PKVIEVIRHP--KDKAESYNPDSALSKEDEERYOKLVITENEOLRLITQKEKIRVLQ 788
Db 738 PKMRRLITRGWQSEADTMKTGSTNNNEEKSRLLEKENRELEKIIAEKERVSELR 797
QY 789 RLVER 793
Db 798 QLQSR 802

RESULT 2
US-09-793-139-55
; Sequence 55, Application US/09793139
; Patent No. US20020156265A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Kenneth A
; TITLE OF INVENTION: DNA Encoding A GABA BR2 Polypeptide And Uses Thereof
; FILE REFERENCE: 54002epctus
; CURRENT APPLICATION NUMBER: US/09/793,139
; CURRENT FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Rattus Sp.
US-09-793-139-55

Query Match 46.5%; Score 2032; DB 9; Length 844;
Best Local Similarity 49.1%; Pred. No. 7.4e-172;
Matches 388; Conservative 151; Mismatches 213; Indels 38; Gaps 9;

QY 23 SPHLQGVAGRDP-----ELHIGGIFPIAGKGWOGWGQACMPATRLALDDVNK 70
Db 32 SPHLP-----RPHPRVPPHPSERRAVYIGALFPMS--GGWPGGQACQPAVEMALDVNS 84
QY 71 QPNLLPGFKLILHNSDECPGLGASVMYNLLYNKPOKMLLAGCSTVCTVVAEAKMN 130
Db 85 RRDILPDYELKLIHDSKCDPGQATKLYLYELLNDPIKIIIMPFGCSVSTLVAEAAKMN 144
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QY 131 LIVLYCASSPALSDRKRFPTLFRTHPSATVHNPTRIKMKKFGWSRVAILLOQAEVFI 190
Db 145 LIVLYSGSSPALSNRQRFPTFFTHPSATLHNPTRVKLFKEKWKXKATIQOTTEVFTS 204
QY 191 TVEDLENRCMEAGVEIVTROSFLSDPTDAVRNLRQDARIIVGLFYVVAARVLCMEYKO 250
Db 205 TLDDLERVKEAGIEITFRQSFSDPAPVKNLRODARIIVGLFYETEARKEVCEVKE 264
QY 251 QLYGRAHVFFIGWYEDNWEVNLKAGIEITCIVQMRITAEAGHLITTEALMNNQNTTIS 310
Db 265 RLFGKVVWFLIGWADNWKFI--YDPSINCTVDEMTAEVGHITTEIVMLNPANTRIS 322
QY 311 GMTAEERHRLNQAALIEEGYDINHRYPE---GYQEPALAYDAVWSVALAANKTKMERLIT 367
Db 323 NMTSQEVEKLTIKRL-----KRHPEETGGFQEPALAYDAIWAALALANKTSGGG 373
QY 368 GKSLRDTYTDKIEADEIYAAMSTOFLGSGVVAFFSSOGDRIALTOIEOMIDGKYEL 427
Db 374 SGVRLDFNNTQITDOIYRAMSSSEFGVGHVFDASGRNWTILIEOLOGGYSYKI 433
QY 428 GYDTOLDNLISWLNTEOWIGKVPQDRTIVPHVLTIVSLPLFVCMCTISSCGIFVAFALI 487
Db 434 GYDSTKDDLWSKTDKWIGSPPADQTLVTKTFRFLSOKLFISVSVLSLGLVAVVCL 493
QY 488 IFNIWKHRRVIOSSHVPVCNTIMLFGVILICISVILLGIDGRFVSPPEYKICQARAWLL 547
Db 494 SFNIYNSHVRYIQNSQPNLNLTAAGCSLAAVFPPLGIDGYHIGRNQFPFVCOARLWLL 553
QY 548 STGETLAYGAMFSKVRVHRETTK--AKTDPKKKVPEPKLYTMVSGLLSIDLVILLSQOI 605
Db 554 GLGSLGYGSMTKIWWVHTTKKEKKEKWKTLPEPKLYATVGLLVGMDVLTALWQI 613
QY 606 FDPQRYLETFLPDPVSTDDIKIRPELEHESORNSMWLGLVYGFGLIIVFLGFLAY 665
Db 614 VDLPHRTIETFAKEEPREDI--DVSILPOLEHCSRKMTWLGIYGYKGLLLGIFLAY 672
QY 666 ETRSIKYKQINDSRVYGMISYVNVVLCITAPVGMVIAASQODASFVAFVALAIFCCFLSM 725
Db 673 ETKSVSTEKINDHRAVGMAYINVAVLCITAPVTMILSSQODAAFAFASLAIVFSSYITL 732
QY 726 LLIFVPKVIEWIRHPKDKAESK--YNPDSALSKEDEERYOKLVITENEOLRLITQKEKI 783
Db 733 VLFVPMRRLITRGWQSEADTMKTGSTNNNEEKSRLLEKENRELEKIIAEKERV 792
QY 784 RVLRLRVER 793
Db 793 SELRHQLQSR 802

RESULT 3
US-09-818-879-55
; Sequence 55, Application US/09818879
; Patent No. US20010023289A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Kenneth
; APPLICANT: Laz, Thomas
; APPLICANT: Borowsky, Beth
; TITLE OF INVENTION: DNA encoding a GABABR2 polypeptide and uses thereof
; FILE REFERENCE: 1795/54002DA
; CURRENT APPLICATION NUMBER: US/09/818,879
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/211,755
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Artificial/Unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(844)
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; OTHER INFORMATION: PEPTIDE  
US-09-818-879-55

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Query Match          46.5%; Score 2032; DB 10; Length 844;
Best Local Similarity 49.1%; Pred. No. 7.4e-172;
Matches 388; Conservative 151; Mismatches 213; Indels 38; Gaps 9;

QY 23 SPHLOGGVAGRPD-----ELHIGGIPPIAGKGWGGQACMPATRLALDDVVK 70
Db 32 SPHLP-----RPHRPVPHPPSSERRAVYIGALFPMs--GGWPGQACQPAVEMALDDVNS 84

QY 71 QPNLLPGFKLLIHSNDSECEPGLGASVMYLLYKPKQLMLLAGCSTVCTTVAEAAKMN 130
Db 85 RRDILPDYELKLIHDSKCDPGQATKYLYELLNDPIKILMPGCSSTVLVAEAAKMN 144

QY 131 LIVLYGASSPALSDRKRPFTLFRTHPSATVHNPTRIKLMKFGSRVAILQOAEVEFVS 190
Db 145 LIVLSYSSSPALSNRQRFPTFRTHPSATLHNPTRVKLFKWKWKIATIQOTTEVTS 204

QY 191 TVEDLENRCMEAGVEIVTQSFSLSDPTDAVNLRRQDARIIVGLFYVVAARRVLCMYKQ 250
Db 205 TLDLEERVKEAGIEITFRQSFSDPAVPVKNLKRQDARIIVGLFYETEARKVFCVYKE 264

QY 251 QLYGRAHWFFICGWEEDNMYEVLNKAEGITCTVEQMRITAEAGHLTTEALMNNQNTTIS 310
Db 265 RLFGKKYVWFLIGWYADNFKT--YDPSINCTVEEMTEAVEGHITTEIVMLNPANTRSTS 322

QY 311 GMTAEFRHLNQAOLIEEGYDINHRYPE---GYQEAPLAYDAVMSVALAFNKTMERLTT 367
Db 323 NMTSQEFVEKTKRL-----KRHPETGGFQEAPLAYDAIWAALALNKTSGGGR 373

QY 368 GKSLRDTFTYDKEIADEIYAAMNSTQFLGVSQVAFSSQGDRIALTQEQMIDGKYKL 427
Db 374 SGVRLEDFNYNNQITDQIYRAMNSSFEVGHVVDASGRMAWTLIEQLQGGSYKKI 433

QY 428 GYDTQDLNLSWLTBOWIGGKVPQDRTIVTHVLRVSLPLFVCMCTISSCGIFVAFALI 487
Db 434 GYDSTKDDLSWSTDKWIGGSPADQTLVIKTRFSLQKLFISVSVLSGLIVLAVVCL 493

QY 488 IFNIWNKRRVIOSSHVPVCNTIMLFGVVICLSVILLGIDGRFVSPEEYPKICQARWLL 547
Db 494 SFNIYNSHVRIQNSQPNLNLTAVGCSLAAVFPGLDGYHIGRSQFPFVQCARWLL 553

QY 548 STGTFLAYGAMFSKVRVHRFTTK--AKTDPKKKVPKLYTMVSGLLSIDVILLSQOI 605
Db 554 GLGFSLYGSMFTKIWWVHTVFTKKEKKEWRKTLPEPKLYATVGLLVGMDVLTIAWQI 613

QY 606 FDPQRYLETFPLEDDPVTSTDDIKIRPELEHCESSQNSMWGLVYGFKGLILVFLGLAY 665
Db 614 VDLPHRTIETFAKEEKEDI-DVSILPQLEHCSKKMNTWLGIFYGKGLLLGLIFLAY 672

QY 666 ETRSIKVKQINDSRVGMISYNNVVLCLITAPVGMVIAQQDASFAFVALAVIFCCFLSM 725
Db 673 ETKSVSTEKINDHRAVGMAYINAVLCLITAPVTMLSSQDAAAFASIAIVFSSYITL 732

QY 726 LLIFVPKVIETIRHPKDAESK--YNPDSAIKDEERYOKLVTEQORLITQKEEKI 783
Db 733 VVLFVPMRRLITRGEWQSETQDTMTKGSSTNNNEEKSRLLEKENRELEKIIAEKEERV 792

QY 784 RVLQRQLVER 793
Db 793 SELRHQLQSR 802
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## RESULT 4

US-09-211-755B-55  
Sequence 55, Application US/09211755B  
Patent No. US20020045742A1  
GENERAL INFORMATION:  
APPLICANT: Kenneth A. Jones, Thomas M. Laz, Beth Borowsky  
TITLE OF INVENTION: DNA Encoding a GABAR2 Polypeptide And Uses Thereof  
FILE REFERENCE: 1795/54002-D  
CURRENT APPLICATION NUMBER: US/09/211.755B

## RESULT 5

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; CURRENT FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 09/186.664
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 844
; TYPE: PRT
; ORGANISM: RAT;
US-09-211-755B-55

Query Match          46.5%; Score 2032; DB 10; Length 844;
Best Local Similarity 49.1%; Pred. No. 7.4e-172;
Matches 388; Conservative 151; Mismatches 213; Indels 38; Gaps 9;

QY 23 SPHLOGGVAGRPD-----ELHIGGIPPIAGKGWGGQACMPATRLALDDVVK 70
Db 32 SPHLP-----RPHRPVPHPPSSERRAVYIGALFPMs--GGWPGQACQPAVEMALDDVNS 84

QY 71 QPNLLPGFKLLIHSNDSECEPGLGASVMYLLYKPKQLMLLAGCSTVCTTVAEAAKMN 130
Db 85 RRDILPDYELKLIHDSKCDPGQATKYLYELLNDPIKILMPGCSSTVLVAEAAKMN 144

QY 131 LIVLYGASSPALSDRKRPFTLFRTHPSATVHNPTRIKLMKFGSRVAILQOAEVEFVS 190
Db 145 LIVLSYSSSPALSNRQRFPTFRTHPSATLHNPTRVKLFKWKWKIATIQOTTEVTS 204

QY 191 TVEDLENRCMEAGVEIVTQSFSLSDPTDAVNLRRQDARIIVGLFYVVAARRVLCMYKQ 250
Db 205 TLDLEERVKEAGIEITFRQSFSDPAVPVKNLKRQDARIIVGLFYETEARKVFCVYKE 264

QY 251 QLYGRAHWFFICGWEEDNMYEVLNKAEGITCTVEQMRITAEAGHLTTEALMNNQNTTIS 310
Db 265 RLFGKKYVWFLIGWYADNFKT--YDPSINCTVEEMTEAVEGHITTEIVMLNPANTRSTS 322

QY 311 GMTAEFRHLNQAOLIEEGYDINHRYPE---GYQEAPLAYDAVMSVALAFNKTMERLTT 367
Db 323 NMTSQEFVEKTKRL-----KRHPETGGFQEAPLAYDAIWAALALNKTSGGGR 373

QY 368 GKSLRDTFTYDKEIADEIYAAMNSTQFLGVSQVAFSSQGDRIALTQEQMIDGKYKL 427
Db 374 SGVRLEDFNYNNQITDQIYRAMNSSFEVGHVVDASGRMAWTLIEQLQGGSYKKI 433

QY 428 GYDTQDLNLSWLTBOWIGGKVPQDRTIVTHVLRVSLPLFVCMCTISSCGIFVAFALI 487
Db 434 GYDSTKDDLSWSTDKWIGGSPADQTLVIKTRFSLQKLFISVSVLSGLIVLAVVCL 493

QY 488 IFNIWNKRRVIOSSHVPVCNTIMLFGVVICLSVILLGIDGRFVSPEEYPKICQARWLL 547
Db 494 SFNIYNSHVRIQNSQPNLNLTAVGCSLAAVFPGLDGYHIGRSQFPFVQCARWLL 553

QY 548 STGTFLAYGAMFSKVRVHRFTTK--AKTDPKKKVPKLYTMVSGLLSIDVILLSQOI 605
Db 554 GLGFSLYGSMFTKIWWVHTVFTKKEKKEWRKTLPEPKLYATVGLLVGMDVLTIAWQI 613

QY 606 FDPQRYLETFPLEDDPVTSTDDIKIRPELEHCESSQNSMWGLVYGFKGLILVFLGLAY 665
Db 614 VDLPHRTIETFAKEEKEDI-DVSILPQLEHCSKKMNTWLGIFYGKGLLLGLIFLAY 672

QY 666 ETRSIKVKQINDSRVGMISYNNVVLCLITAPVGMVIAQQDASFAFVALAVIFCCFLSM 725
Db 673 ETKSVSTEKINDHRAVGMAYINAVLCLITAPVTMLSSQDAAAFASIAIVFSSYITL 732

QY 726 LLIFVPKVIETIRHPKDAESK--YNPDSAIKDEERYOKLVTEQORLITQKEEKI 783
Db 733 VVLFVPMRRLITRGEWQSETQDTMTKGSSTNNNEEKSRLLEKENRELEKIIAEKEERV 792

QY 784 RVLQRQLVER 793
Db 793 SELRHQLQSR 802
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Db 681 FTKLWVHTVTFTKEEKKERWKLTLEPKKLYATGVLGLGMVDVLTAIWQIVDPLHRTIETF 740
QY 617 PLEDPVSTTDIKIRPELECHESORNSMWLGVLGVFGKLILVFLGLFAYETRSIKVKQLN 676
| : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 741 AKEEPKEDI-DVSILPOLEHCSSRKMNTWLGIPIGYKGLLLIGIFLAYETKSVSTEKIN 799
QY 677 DSRVVGMSIYNVVLCITAPVGVMIAQQOASDAFAFVALAVIFCCFLSMILLIFVPKVIEV 736
| : | ||||| | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 800 DHRAVGMAIYNVAVLCITAPVTMILSSQDDAAAFAPASLAIVFSYITLVLVFPKMRL 859
QY 737 IRHP--KDKAESKNPDOSAISKDEDERYQKLV TENOLQRLTQKEEKIRVLQR LVER 793
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 860 ITRGEWSQAQDTMKTGSSTNNNEEEKSRLEKENRELEKIIAEKEERVSELRHQLQSR 918

RESULT 7
US-09-875-724-4
; Sequence 4, Application US/09875724
; Patent No. us2002091250A1
; GENERAL INFORMATION:
; APPLICANT: Kaupmann, Klemens
; APPLICANT: Bettler, Bernhard
; APPLICANT: Bittiger., Helmut
; APPLICANT: Frost, Wolfgang
; APPLICANT: Mickel, Stuart J
; TITLE OF INVENTION: Metabotropic GABA[B] Receptors, Ligands and their uses
; FILE REFERENCE: 4-20876/A/PCT
; CURRENT APPLICATION NUMBER: US/09/875,724
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/194,382
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 793
; TYPE: prt
; ORGANISM: Homo sapiens
; US-09-875-724-4
```

```

Qy 454 RTIVTHVLRVTSLPLFVCMCTCISSCGFIAPFALIIFNWKNHRRVYQSHPVCNTIMLFG 513
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 409 QTLVIKTFRELSQKLFIISVLSGLGTVLA VVCLSFNIYNSHRYIQNSQPNIJNLTAVG 468
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Qy 514 VIICLSIILGIDGRFVSPEYPKICQARAWLLSTGFTLAYGAMFSKVVRHVRFETK-- 571
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 469 CSLAAVAFFPUGLOGYHIGRNQFPVCOARUWLGLGFSIGYSMFTKIWWHTVTTKKE 528
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Qy 572 AKTDPKKKVPWKLYTWVSGILLSIDLVLISWQIFDPLQRYLETFLPLEDPVSTDDIKIR 631
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 529 EKKEMRKTLPWKLYATVGLLVGMVDVLTAIQVLDPLHRTIETFAKEEPKEDI-DVSIL 587
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Qy 632 PELCHCSQRNSMWLGIVGFKGILLVFGLFLAYETRISKVKQINDSRYYVMGSINYVVVL 691
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 588 PQLEHCSSRKMTNLGIFYGYKGLLLGLGIFLAYETKSVESTEKINDHRAGMAIYNNAVL 647
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Qy 692 CLITAPGVMTASOODASFAPVALAVIFCCFLSMLLIFFVPKVIEWIRHP--KDKAESKYN 749
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 648 CLITAPVTMIUSSOODAFAFASIAVFSSYITLVLFVPKMRLRLTRGEQWSEAOOTMK 707
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Qy 750 PDSAISKEDEERYOKLYTENEQLRQLTQKEKRIVLRQRLVER 793
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 708 TGSSTNNNEEKSRLLENKENRELEKIIAEKEERVELRHQLQSR 751
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |

RESULT 8
US-09-211-755B-56
; Sequence 56, Application US/09211755B
; Patent No. US20020045742A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth A. Jones, Thomas M. Laz, Beth Borowsky
; TITLE OF INVENTION: DNA Encoding a GABABR2 Polypeptide And Uses Thereof
; FILE REFERENCE: 1795/54002-D
; CURRENT APPLICATION NUMBER: US/09/211,755B
; CURRENT FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 09/186,664
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 960
; TYPE: PRNT
; ORGANISM: RAT;
US-09-211-755B-56
```

Query Match 46.4%; Score 2029.5; DB 10; Length 793;  
Best Local Similarity 49.9%; Pred. No. 1.1e-171;  
Matches 381; Conservative 151; Mismatches 211; Indels 21; Gaps 7;

	QY	379	DKEIADBIYAAMNSTOFLGVSGVVAFFSSOGDRIALFOIEOMIDGKYEKLYGYDYDTOLDNLUS	438
			: :   :	
	Db	501	NOTITDQIRAMNSSPEFGYSGHWFDAGSRMAWTLIEQLGGSYKKIYYDSTKDULS	560
			: :   :	
	QY	439	WLNTEQWIGGKVPODRTIIVTHVLTVSLPLFVCMCHTISSCGFVFAPALLIFNIWNKHRRV	498
			: :   :	
	Db	561	WSKTDKWIGGSPPADOTLVTKTRFTLSQKLFIISVSLLSIGIVLAVVCVLSFNINSHVRV	620
			: :   :	
	QY	499	IQSSHPCVNTIMLFVGVTICILSVILLGIDGRFVSPEEYPKICOARAWLLSTGFTLAYGAM	558
			:   :	
	Db	621	IQNSQPNNLTAVGCSLAALAAVPJGLDGYHIGRSQFPFCVQARUMLLGLGFSLGYSGM	680
			:   :	
	QY	559	FSKWRVHRHTTK--AKTPDKKVEPWKLTYMSGLLSIDLVTLLSQWDFDPLORYLETF	616
			:   :	
	Db	681	FTKIWWVHTVTTKEEKKEWKRTLEPKLYATVCLLVGMDVLTIAIWQIVDPDHRTIEFF	740
			:   :	
	QY	617	PLEDPVSTTDIIKIRPELEHCESORNMWGLGVYKGILLVFGFLAYETRSIKVKQIN	676
			:   :	
	Db	741	AKEPKEDI-DVSIILPOLCHCCKKNMTWLGIFYGYKGLLLLGIPLAYETSKVSTEKIN	799
			:   :	
	QY	677	DSRYVMGSINYVVLCILITAPVGMWTASOODASFVALAVIPCCFLSMILIFVPKVIEW	736
			:   :	
	Db	800	DHRAVGMAIYNVAVLCILITAPVTMLISSOODAFAFASLAIVESSYITLWLVFVKMREL	859
			:   :	
	QY	737	IRHPDKAESK--YNPDSAISKEDERYOKLV TENEQRLTOKEKIRVLRQRILVER	793
			:   :	
	Db	860	ITRGWQSETQDMTKTGTSSTNNNEEKSRLLKENRELEKIITAEKEERVELSRHQLSR	918
			:   :	
		RESULT 9		
		US-09-875-724-2		
		; Sequence 2, Application US/09875724		
		; Patent No. US20020091250A1		
		; GENERAL INFORMATION:		
		; APPLICANT: Kaupmann, Klemens		
		; APPLICANT: Bettler, Bernhard		
		; APPLICANT: Bittiger, Helmut		
		; APPLICANT: Frost, Wolfgang		
		; APPLICANT: Mickel, Stuart J		
		; TITLE OF INVENTION: Metabotropic GABA[B] Receptors, Receptor-specific		
		; TITLE OF INVENTION: Ligands and their uses		
		; FILE REFERENCE: 4-20876/A/PCT		
		; CURRENT APPLICATION NUMBER: US/09/875,724		
		; CURRENT FILING DATE: 2001-06-06		
		; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/194,382		
		; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-25		
		; NUMBER OF SEQ ID NOS: 8		
		; SOFTWARE: PatentIn Ver. 2.0		
		; SEQ ID NO 2		
		; LENGTH: 960		
		; TYPE: PRT		
		; ORGANISM: Rattus norvegicus		
		US-09-875-724-2		

Query Match	46.4%	Score 2029.5;	DB 10;	Length 960;
Best Local Similarity	49.4%;	Pred. No. 1.5e-171;		
Matches 385;	Conservative 152;	Mismatches 171;	Indels 23;	Gaps 8;
QY	24	PHLGGVAGRDE--LHIGGIFFIAGKGGWGGGQACMPATRLALDDVNKQPNLLPFGKLI	81	
DB	154	PHCOVNPTHSERRAVYIGALFPMs--GGWPGGQACQAPVEMALEDVNSRRDILPDYELK	211	
QY	82	LHNSDSCPCGLGASVMYNLLYNKQKMLLAGSCVTCVTVAEAAKMWNLIVLCYGASSP	141	
DB	212	LIHSDKCDPGQATKYLYELLYNDPIKIILMPGCSSTVLAEEARMWNLIVLYGSSSP	271	
QY	142	ALSDKRFPPTLFRTHPSATVHNPTRIKLWKFGNSRVAILLQOAEVFSTTVEDEDNCME	201	
DB	272	ALSNRQRPPTFRTHPSNTLHNPTRVKLFKAWGKKIATIQOTTTEVFTSTLDDLEERVEK	331	
QY	202	AGVEITVRSQSLSDPTDAVRNLRRQDARIIVGLFVYVAARVLCVMYKQOYLGRAHVWFF	261	
DB	332	AGIEITVRSQSPDPVVKMLKQDARIIVGLFVEEARKVFCVEYKRGKGYVWFL	391	

Qy	262	IGWYEDNNYEVN	KAEGTCTCTVEQMRIAAGHLTTEALWMNONNOTTISGMTAEFRRL	321
Db	392	IGWYADNNFKT	--YDPSINCTVEEMTEAVEGHTEIIVMLNPANTRSINMTSQBEVFKL	449
Qy	322	NOALIEEGYDINH	DHRYPE--CYOEAPLAYDAVWSVALAFNKTMERLTGKKSLRDTY	378
Db	450	TKRL-----	KRHPETGGQAPLAYDAIMALALANKTSGGGRSGVRLDEDFYN	500
Qy	379	DKEIADEIYAAMN	STOFLGVSQVAFSSQGDRIALTQIEQMTDGYEKYELGYDTOLDNLS	438
Db	501	NOTITDQIYRAMN	SSFEVSGSHVVDASGRMAWTLIEQLGGSYKKIYGYDSTKDDL	560
Qy	439	WUNTEQWIGKVP	QDRTIVTVHLRVSLPLFCVCMCTISCCGIFAFALIIFNINWKHRY	498
Db	561	WSKTDKWIQGGP	PADOTIVIKTFRLSKLFISVLSGLGIVLAVVCLSFNIYNSHRY	620
Qy	499	IQSSHPVCNTIM	FGVVICLSVILGIDGRVSPPEEYPKICQARAWLLSTGFTLAYGAM	558
Db	621	IQNSOPNLNLT	AVGCSLALAAVFLGIDGYHIGRSQPFVCOARLWLLGFGSLCYGSM	680
Qy	559	FSKYWRVHRFTK	--AKTDPKKVPEWKLYTMVSGLLSIDLVLLSWOIFDPLQRYLETF	616
Db	681	FTKIMWHTVTF	KKEKKWKRLTEPWLKYAVVGLLVGMDVLTIAIWQIVDPLHRTIETF	740
Qy	617	PLEDPVITTDIK	IRPELEHCESORNMWGLVYFGKGLLVFLAYETPSIKVKQIN	676
Db	741	AKEEPKEDI	-DVSILPOLHEHCSSKMMTWLGYGYKGLLLGLGIFLAYETKSVSTEKIN	799
Qy	677	DSRYVGMSTYNN	VVLCLITAPVGMVIASSQDAFALAVAFICFCLSMILIFVPEKVIEW	736
Db	800	DHRVGMALYNN	VAVLCLITAPVTMILSSQDAAFASIAIVFSSVITLVVLVFPKMRRL	859
Qy	737	TRHPKDKAESK	--YNPDSAISKEDEERYOKLVTEENOQLRITQKEEKIRVURQRLIVER	793
Db	860	ITRGWQSETQD	TMTKGTSGSTNNNEEEKSRLEKENREKIIAEKEERYSELRHOLQSR	918
RESULT 10				
US-09-793-139-47				
; Sequence 47, Application US/09793139				
; Patent No. US20020156265A1				
; GENERAL INFORMATION:				
; APPLICANT: Jones, Kenneth A				
; TITLE OF INVENTION: DNA Encoding A GABA BR2 Polypeptide And Uses Thereof				
; FILE REFERENCE: 540026ptcus				
; CURRENT APPLICATION NUMBER: US/09/793,139				
; CURRENT FILING DATE: 2001-02-26				
; NUMBER OF SEQ ID NOS: 55				
; SOFTWARE: PatentIn Ver. 2.1				
; SEQ ID NO 47				
; LENGTH: 941				
; TYPE: PRT				
; ORGANISM: Homo Sapiens				
US-09-793-139-47				
Query Match 29.5%; Score 1290; DB 9; Length 941;				
Best Local Similarity 33.9%; Pred.No.6.1e-106;				
Matches 286; Conservative 170; Mismatches 332; Indels 56; Gaps 18;				
Qy	18	LCLIASPHLQGV	AGRP-----DELHIGGIPPI---AGKGWGQGGQACMPATRLALDDV	68
Db	31	LLLPLAGWAGW	ACRAPPPSPPLSINGLMLPLTKEVAKGSI--GRGVLPVAVELAIQI	88
Qy	69	NKQPNLLPGFK	LILHNSDECEPGIGASVWYNLLYNKPKMLLAG-CSTVCTTVAEAAK	127
Db	89	RNESLLRPYF	-LDRLXDTECNKAGLRAFYDAIKYGPNNHLMVFGVCPVSVTSIIAESLQ	147
Qy	128	MKNLIVLCYG	ASSPALSDEKREPTFLTRHPSPATVNPTRIKLMKKFGHRSVAILQAAEV	187
Db	148	GNNVLQSFATP	TVLADKKKYPYFRFTVPSDNVNPAILKLLKHQYQMKRVGLTQDVOR	207
Qy	188	FISTVEDLENRC	MEAGVETVTRQSFSLSDPTDAVRLRRDARIIVGLFVYVAARVLCEM	247

Db 208 FSEVRNDLTGVLXGEDIESTESFSDNCPCTSVKKLKGNDRVRIILGQFDQNMNAKVFCFA 267  
QY 248 YKOOLYGRAHVFFIGWYEDNWEY-VNLKABGICTVQOMRIAARGHLLTTEALMNNQ 306  
Db 268 YEENYGSKYQWIIIPGWYEPWWEQVHTSEANSSRLKNLLAAMEGYIGVDFEPLSSKQI 327  
QY 307 TTISGMTAEFRHRLNQALIEEGYDINHRYPEGYQEAFLAYDAVMSVALAFNKTMERL- 365  
Db 328 KTISGKTPOQYEREYNKKRSGVPSKFH-----GY-----AYDGIWIAKTLQRAMETLH 377  
QY 366 -TTGKSLRDFTYTDKETADIYAAMNSTQFLGVSQVAFSSQGDRIALTQIEQMIDGKY 424  
Db 378 ASSRHQRIQDFNYDHTLGRILILAMNETNFGVTQGVVFRN-GERMGTIKFTQFQDSRE 436  
QY 425 EKLGYDTQLDNLNLSWLN-TEQWIGKVPQDRITVHLRTVSLPLFVCMCTISSCGIFVA 483  
Db 437 VKGEYNAVADTLEIINDTIRFQSEPPKDKTIIIEQLRKISLPLYSILSALTILGMIMA 496  
QY 484 FALIFNIWKNHRRVIOSSHVPVCMNTIMLFGVILICISVILLGIDGRFVSPPEYKICQAR 543  
Db 497 SAFLEFNKRNQKLIKMSPPYNNLIILGMLSYASIFLGLDGSFVSEKTFETLCTV 556  
QY 544 AMLLSTGFTLAYGAMFSKVRVHRFTTAKTDPKKKVPEWPKLYTMVSGLLSIDLVILLSW 603  
Db 557 TWILTVGYTTAFGAMFAKTRVHAIFKNVKM-KKKIILKQKLLVTVGGMLLIDLCILCW 615  
QY 604 QIFDPLQRYLETFFLE-DPVSTTDDIKIRPELEHCESSQNSMWLGLVYGFGLILVGLF 662  
Db 616 QAVDPLRTVEKYSMEPPAGR--DISIRPLEHCENTHMTIWLGIIVAYVAYGLMLFGCF 673  
QY 663 LAYETRSIKVKQINDSRVGMISYNNVVLCLITAPVGMVIAQQDASFAFVALAVIFCCF 722  
Db 674 LAWETRNVSIPALNDSKYIGMSVYNGIMCIIIGRAVSFLTRQPNVQFCIVALVIFCST 733  
QY 723 LSMLLIFVPKVIEWIRHP-----KDKAESKYNPD-SAIKSEDEERYOKLVT 767  
Db 734 ITLCLVFPVKLITLRTNPDAAQTNRFRQFTQNKEDSKTSTSVTSVNAQASTRLEGLQS 793  
QY 768 ENEQLRLITQKEEKIRVLQRVERGDAKT-----ELNGATGVASAATTSQPA 819  
Db 794 ENHRLRMKITELDKOLEVTMQLQDTPK-KTTYIKQNHQYQELNDILNLFNSTEDGGA 852  
QY 820 SLIN 823  
Db 853 ILKN 856

## RESULT 11

US-09-818-879-47  
; Sequence 47, Application US/09818879  
; Patent No. US2001023289A1  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Kenneth  
; APPLICANT: Laz, Thomas  
; APPLICANT: Borowsky, Beth  
; TITLE OF INVENTION: DNA encoding a GABABR2 polypeptide and uses thereof  
; FILE REFERENCE: 1795/54002A  
; CURRENT APPLICATION NUMBER: US/09/818,879  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR FILING DATE: 1998-12-15  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 47  
; LENGTH: 941  
; TYPE: PRT  
; ORGANISM: human  
US-09-818-879-47

Query Match 29.5%; Score 1290; DB 10; Length 941;  
Best Local Similarity 33.9%; Pred. No. 6.1e-106;  
Matches 286; Conservative 170; Mismatches 332; Indels 56; Gaps 18;

QY 18 LCLIASPHLQGGVAGRP-----DELHIGGIFFI---AGKGGWQGGQACMPATRLALDDV 68  
Db 31 LLLPLAPGAWGARGAPRPPSPPLSLIMGLMLPLTEVAKGSI--GRGVLPAVELALEQI 88  
QY 69 NQPNLLPGFKLILHNSDECEPGLGASVYNNLLYKNPKQLMLLAG-CSTVCTTVAEAK 127  
Db 89 RNESLRLPYF-LDLRLDYTECONAKGLKAFYDAIKYGNHLMVFGVCPSTVSIIEASLQ 147  
QY 128 MNNLIVLCGASSPALSDRKRPEPTLERTHPSATVHPNTRIKLKKMKFGWSVALIQAEEV 187  
Db 148 GWNVLQSLFAATTPVLADKKKYDYFFERTVPSDNVAVPAIILKLLKHQMKRVGTLTQDVQR 207  
QY 188 FISTVEDLENRCMEAGVEIVTQSFSLSDPTDAVNRILRRQDARIIVGLVYVVAARVILCEM 247  
Db 208 FSEVRNDLTGVLXGEDIESTESFSDNCPCTSVKKLKGNDRVRIILGQFDQNMNAKVFCFA 267  
QY 248 YKOOLYGRAHVFFIGWYEDNWEY-VNLKABGICTVQOMRIAARGHLLTTEALMNNQ 306  
Db 268 YEENYGSKYQWIIIPGWYEPWWEQVHTSEANSSRLKNLLAAMEGYIGVDFEPLSSKQI 327  
QY 307 TTISGMTAEFRHRLNQALIEEGYDINHRYPEGYQEAFLAYDAVMSVALAFNKTMERL- 365  
Db 328 KTISGKTPOQYEREYNKKRSGVPSKFH-----GY-----AYDGIWIAKTLQRAMETLH 377  
QY 366 -TTGKSLRDFTYTDKETADIYAAMNSTQFLGVSQVAFSSQGDRIALTQIEQMIDGKY 424  
Db 378 ASSRHQRIQDFNYDHTLGRILILAMNETNFGVTQGVVFRN-GERMGTIKFTQFQDSRE 436  
QY 425 EKLGYDTQLDNLNLSWLN-TEQWIGKVPQDRITVHLRTVSLPLFVCMCTISSCGIFVA 483  
Db 437 VKGEYNAVADTLEIINDTIRFQSEPPKDKTIIIEQLRKISLPLYSILSALTILGMIMA 496  
QY 484 FALIFNIWKNHRRVIOSSHVPVCMNTIMLFGVILICISVILLGIDGRFVSPPEYKICQAR 543  
Db 497 SAFLEFNKRNQKLIKMSPPYNNLIILGMLSYASIFLGLDGSFVSEKTFETLCTV 556  
QY 544 AMLLSTGFTLAYGAMFSKVRVHRFTTAKTDPKKKVPEWPKLYTMVSGLLSIDLVILLSW 603  
Db 557 TWILTVGYTTAFGAMFAKTRVHAIFKNVKM-KKKIILKQKLLVTVGGMLLIDLCILCW 615  
QY 604 QIFDPLQRYLETFFLE-DPVSTTDDIKIRPELEHCESSQNSMWLGLVYGFGLILVGLF 662  
Db 616 QAVDPLRTVEKYSMEPPAGR--DISIRPLEHCENTHMTIWLGIIVAYVAYGLMLFGCF 673  
QY 663 LAYETRSIKVKQINDSRVGMISYNNVVLCLITAPVGMVIAQQDASFAFVALAVIFCCF 722  
Db 674 LAWETRNVSIPALNDSKYIGMSVYNGIMCIIIGRAVSFLTRQPNVQFCIVALVIFCST 733  
QY 723 LSMLLIFVPKVIEWIRHP-----KDKAESKYNPD-SAIKSEDEERYOKLVT 767  
Db 734 ITLCLVFPVKLITLRTNPDAAQTNRFRQFTQNKEDSKTSTSVTSVNAQASTRLEGLQS 793  
QY 768 ENEQLRLITQKEEKIRVLQRVERGDAKT-----ELNGATGVASAATTSQPA 819  
Db 794 ENHRLRMKITELDKOLEVTMQLQDTPK-KTTYIKQNHQYQELNDILNLFNSTEDGGA 852  
QY 820 SLIN 823  
Db 853 ILKN 856

## RESULT 12

US-09-211-755B-47  
; Sequence 47, Application US/09211755B  
; Patent No. US20020045742A1  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth A. Jones, Thomas M. Laz, Beth Borowsky  
; TITLE OF INVENTION: DNA Encoding a GABABR2 Polypeptide And Uses Thereof  
; FILE REFERENCE: 1795/54002-D  
; CURRENT APPLICATION NUMBER: US/09/211,755B  
; CURRENT FILING DATE: 1998-12-15  
; PRIOR APPLICATION NUMBER: 09/186,664

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; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 941
; TYPE: prt
; ORGANISM: human;
US-09-211-755B-47

```

Query Match 29.5%; Score 1290; DB 10; Length 941;  
Best Local Similarity 33.9%; Pred. NO. 6.1e-106;  
Matches 286; Conservative 170; Mismatches 332; Indels 56; Gaps 18;

Db 716 RFQFTQNKEDSKTSTSVTSVQNAQSTSRLEGLQSEHRLRMKITELDKDLDEEVTMQLQD 775  
Qy 793 RGDAGKT-----ELNGATGVASAAVATTSQPASLIN 823  
Db 776 TPE-KTTYIKQNHQYQELNDILNLGNFTSTDDGGKAILKN 813

RESULT 14  
US-09-818-879-2  
; Sequence 2, Application US/09818879  
; Patent No. US20010023289A1  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Kenneth  
; APPLICANT: Laz, Thomas  
; APPLICANT: Borowsky, Beth  
; TITLE OF INVENTION: DNA encoding a GABABR2 polypeptide and uses thereof  
; CURRENT APPLICATION NUMBER: US/09/818,879  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR FILING DATE: US 09/211,755  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 898  
; TYPE: PRT  
; ORGANISM: human  
US-09-818-879-2

Query Match 29.4%; Score 1284; DB 10; Length 898;  
Best Local Similarity 34.2%; Pred. No. 1.9e-105;  
Matches 280; Conservative 169; Mismatches 320; Indels 50; Gaps 17;

Qy 37 LHIGGIFPI---AGKGQGGQACMPATRLALDDVKNQPNLLPGFKLILHNSDSECEPL 93  
Db 13 LSIMGLMPLTKEVAKGSI--GRGVLPAPVELAIEQIRNESLLRPYF-LDLRLYDTECDNAK 69

Qy 94 GASVYVNLNLYNPKQKMLLAG-CSTVCTTVAEAAKMNWNLVLCYGASSPALSDDRKFPTL 152  
Db 70 GLKAFYDAIKYGNHLMVFGVCPSTVTSIIAESLOGNWLQVLSFAATTPVLADKKYPYF 129

Qy 153 FRTHPSATVHNPRIKLMKFGWSRVAILQQAEEVFISTVEDLENRCMEAGVEIVTRQSF 212  
Db 130 FRTVPDNAVNPAILKLLKHQYKRVGTLTQDVQRFSEVRNDLTGVLGEDIETSDTESF 189

Qy 213 LSDPTDAVNRLEQDARIIVGLFYVVAARRVLCMEYKQQLYGRAHVWFIFGWEDNWEY- 271  
Db 190 SNDPCTSVKLLKGNDRVRIILGQFDQNMAAKVFCCAYEENMYGSKYQWIIPGWYPSWWEQ 249

Qy 272 VNLKAEGITCTVEQMRIAEGHLTTEALMNQNNQTTISGMTAEERHRLNQALIEEGYD 331  
Db 250 VHTEANSRCLRNKLLAAMEGYIGVDFEPLSSKQIKTISGKTPQOYEREYNNKRSVGVP 309

Qy 332 INHDYRPEGYOEAPLAYDAVMSVALAFNKTMERL--TTGKSLRDTFTYTDKEIADEIYAA 389  
Db 310 KFH-----GY-----AYDGIWIAKTQRAMETLHASSRHQRIQDNFTDHLGRILNA 359

Qy 390 MNSTQFLGVGVAFSSQGDRIALTQIQDMIDGKYEKIGYDQTQDNLISWLN-TEQWIGG 448  
Db 360 MNETNFFGVGTQGVVFRN-GERMGTIKFTQFQDSREVKGVEYNADVTLEIINDTIRFQGS 418

Qy 449 KVPQDRTIVHTRVSLPLFVCMCTISSCGIFVAFALIINWKNHRRVIOSSHPVCNT 508  
Db 419 EPPKDKTIILEQLRKISLPLYSILSALTILGMIMASAFLEFNNKRNOKLIKMSPPMNN 478

Qy 509 IMLFGVITCLISVLLGIDGRFVSPEEYPKICQARWLLSTGFTLAYGAMFKSVKRVHFR 568  
Db 479 LIILGGMLSYASIEFLGDLGSFVSEKTFETLCTVTRTWLTGVYTTAFGAMFAKTRVHAI 538

Qy 569 TTKATDPKKVPEWPKLYTMVSGLSLIDLVILLSQVIFDPQLQRYLETFFLE-DPYSTTDD 627  
Db 539 FKNVKM-KKKIKQKLLVIGVGMILLIDLCILICQAVDPLRRRTYKYSMEPDPAQR--D 595

Qy 628 IKIRPELEHCESSORNSMWLGLVYGFKGLIILVFLFLAYETRSIKVKOINDSRVGMYSIN 687  
Db 596 ISIRPLEHECNHMTIWLGIYAYKGLMLFCFLAWETRNYSIPALNDSKYIGMSYIN 655

Qy 688 VVVLCLITAPVGMVIAQQDASFAFVALAVIFCCFSLMILLIFVPKVIETVRHP----- 740  
Db 656 VGIMCIIGAASFLTRDQPNWQFCIVALVILFCSITILCLVFPKILITLNTDFDAQNR 715

Qy 741 -----KDKAESKYNPD-SAISKEDEERYQKLVTEQQLRLITQKEEKIRVLQRQIVE 792  
Db 716 RFQFTQNKEDSKTSTSVTSVQNAQSTSRLEGLQSEHRLRMKITELDKDLDEEVTMQLQD 775

Qy 793 RGDAGKT-----ELNGATGVASAAVATTSQPASLIN 823  
Db 776 TPE-KTTYIKQNHQYQELNDILNLGNFTSTDDGGKAILKN 813

RESULT 15  
US-09-211-755B-2  
; Sequence 2, Application US/09211755B  
; Patent No. US20020045742A1  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth A. Jones, Thomas M. Laz, Beth Borowsky  
; TITLE OF INVENTION: DNA Encoding a GABABR2 Polypeptide And Uses Thereof  
; FILE REFERENCE: 1795/54002-D  
; CURRENT APPLICATION NUMBER: US/09/211,755B  
; CURRENT FILING DATE: 1998-12-15  
; PRIOR APPLICATION NUMBER: 09/186,664  
; PRIOR FILING DATE: 1998-11-04  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 898  
; TYPE: PRT  
; ORGANISM: HUMAN;  
US-09-211-755B-2

Query Match 29.4%; Score 1284; DB 10; Length 898;  
Best Local Similarity 34.2%; Pred. No. 1.9e-105;  
Matches 280; Conservative 169; Mismatches 320; Indels 50; Gaps 17;

Qy 37 LHIGGIFPI---AGKGQGGQACMPATRLALDDVKNQPNLLPGFKLILHNSDSECEPL 93  
Db 13 LSIMGLMPLTKEVAKGSI--GRGVLPAPVELAIEQIRNESLLRPYF-LDLRLYDTECDNAK 69

Qy 94 GASVYVNLNLYNPKQKMLLAG-CSTVCTTVAEAAKMNWNLVLCYGASSPALSDDRKFPTL 152  
Db 70 GLKAFYDAIKYGNHLMVFGVCPSTVTSIIAESLOGNWLQVLSFAATTPVLADKKYPYF 129

Qy 153 FRTHPSATVHNPRIKLMKFGWSRVAILQQAEEVFISTVEDLENRCMEAGVEIVTRQSF 212  
Db 130 FRTVPDNAVNPAILKLLKHQYKRVGTLTQDVQRFSEVRNDLTGVLGEDIETSDTESF 189

Qy 213 LSDPTDAVNRLEQDARIIVGLFYVVAARRVLCMEYKQQLYGRAHVWFIFGWEDNWEY- 271  
Db 190 SNDPCTSVKLLKGNDRVRIILGQFDQNMAAKVFCCAYEENMYGSKYQWIIPGWYPSWWEQ 249

Qy 272 VNLKAEGITCTVEQMRIAEGHLTTEALMNQNNQTTISGMTAEERHRLNQALIEEGYD 331  
Db 250 VHTEANSRCLRNKLLAAMEGYIGVDFEPLSSKQIKTISGKTPQOYEREYNNKRSVGVP 309

Qy 332 INHDYRPEGYOEAPLAYDAVMSVALAFNKTMERL--TTGKSLRDTFTYTDKEIADEIYAA 389  
Db 310 KFH-----GY-----AYDGIWIAKTQRAMETLHASSRHQRIQDNFTDHLGRILNA 359

Qy 390 MNSTQFLGVGVAFSSQGDRIALTQIQDMIDGKYEKIGYDQTQDNLISWLN-TEQWIGG 448  
Db 360 MNETNFFGVGTQGVVFRN-GERMGTIKFTQFQDSREVKGVEYNADVTLEIINDTIRFQGS 418

Qy 449 KVPQDRTIVHTRVSLPLFVCMCTISSCGIFVAFALIINWKNHRRVIOSSHPVCNT 508  
Db 419 EPPKDKTIILEQLRKISLPLYSILSALTILGMIMASAFLEFNNKRNOKLIKMSPPMNN 478

QY	509	IMLFGVILCLISVILGIDGRFVSPEXPKICQARAWLLSTGETLAYGAMFSKVWRVHRF	568
Db	479	LIILGMLSYASIFLFGDGSFVSEKTFETLCTVRTWILTGYTTFAGAMFAKTWRVHAI	538
QY	569	TTKAKTDPKKVPEPWKLYTMVSGLLSIDIVILLISWQIFDPLQRYLETFPLE-DPVSTTDD	627
Db	539	FNKVM-KKKIIKDQKLLVIVGGMLLIDLCILICWQAVDPLRRTVEKYSWEPPAGR--D	595
QY	628	IKIRPELEHCESORNSMWGLVYGFKGLILVFLFLAYETRISIKVKQINDSRVYGMISIYN	687
Db	596	ISIRPLEHCENTHMTIWLGIIVAYKGLLMFLGCFLEWETRNVSIPALNDSKYIGMSVYN	655
QY	688	VVVLCLITAPVGMVIASQODASFAFVALAVIFCCFLSMLLI FVPKVIEWIRHP-----	740
Db	656	VGIMCIIGAASFTRDQPNVQFCIVALVIFCSTITLCLVFPVKLITLTNPDAATQNR	715
QY	741	-----KDKAESKYNPD-SAISKEDEERYQKLVTENEOLQRLITOKEEKIRVLRORLVE	792
Db	716	RQFTQNKKEDSKTSTSVTSYNQASTSRLEGLOSNNHRLRMKITELDKDEEVTWOLQD	775
QY	793	RGDAKGT-----ELNGATGVASAAVATTSPASLIN	823
Db	776	TPE-KTTYIKONHYOELNDILNLFNFTSTDGGKAILKN	813

Search completed: November 19, 2002, 10:52:13  
Job time : 15 secs

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:11:13 ; Search time 21 Seconds  
(Without alignments)  
3046.982 Million cell updates/sec

Title: US-09-715-962-2  
Perfect score: 4374  
Sequence: 1 MRKDWTSDBGVTFWIFLLCL.....LINSSAHATPAATLAIQTQE 840

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %	Length	DB ID	Description
1	2024.5	46.3	960	2 JE0356	gamma-aminobutyric
2	457	10.4	402	2 T29703	hypothetical prote
3	356.5	8.2	912	2 JH0583	metabotropic gluta
4	355	8.1	908	2 I49142	metabotropic gluta
5	353	8.1	915	2 A49874	metabotropic gluta
6	342	7.8	879	2 JC7160	metabotropic gluta
7	334.5	7.6	871	2 A46742	metabotropic gluta
8	333	7.6	879	2 JH0562	metabotropic gluta
9	318	7.3	872	2 JH0561	metabotropic gluta
10	303.5	6.9	1171	2 A42916	metabotropic gluta
11	303	6.9	1218	2 S71376	glutamate receptor
12	302.5	6.9	1180	2 JC2132	metabotropic gluta
13	297.5	6.8	1212	2 JC2131	metabotropic gluta
14	294	6.7	999	2 T27628	hypothetical prote
15	268	6.1	1199	2 A41939	G protein-coupled
16	232.5	5.3	976	2 T51137	ionotropic glutama
17	219.5	5.0	1078	2 A56715	calcium receptor (
18	219	5.0	941	2 T51135	ligand-gated chann
19	213.5	4.9	1088	2 B56715	calcium receptor (
20	212.5	4.9	1079	2 I59362	calcium/polyvalent
21	212	4.8	1267	2 T21340	hypothetical prote
22	211.5	4.8	925	2 T06128	hypothetical prote
23	211.5	4.8	962	2 D86186	hypothetical prote
24	201.5	4.6	912	2 T51131	ligand gated chann
25	198.5	4.5	1085	2 S40476	Ca(2+)-sensing rec
26	193.5	4.4	551	2 T30806	metabotropic gluta
27	190.5	4.4	923	2 F84732	probable ligand-ga
28	189.5	4.3	953	2 F84732	probable ligand-ga
29	187	4.3	502	2 S69331	natriuretic peptid

30 186.5 4.3 921 2 T51136  
31 186.5 4.3 925 2 T51133  
32 186.5 4.3 951 2 T51132  
33 185.5 4.3 1140 2 T24213  
34 185.5 4.2 975 2 A84550  
35 184.5 4.2 1047 1 OYRTBR  
36 181.5 4.1 1047 2 I45882  
37 180 4.1 1056 2 T33167  
38 179 4.1 253 2 T29704  
39 178.5 4.1 500 2 E72687  
40 177.5 4.1 1047 1 OYHUBR  
41 175 4.0 1005 2 S33525  
42 172 3.9 1050 2 S45636  
43 169 3.9 950 2 T51134  
44 167.5 3.8 1143 2 T28129  
45 163 3.7 1525 1 A56699

## ALIGNMENTS

RESULT 1

JE0356  
gamma-aminobutyric acid receptor B precursor - human  
N: Alternate names: GABA(B) receptor  
C: Species: Homo sapiens (man)  
C: Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 12-Feb-1999  
C: Accession: JE0356  
R: Grifa, A.; Totaro, A.; Rommens, J.M.; Carella, M.; Roetto, A.; Borgato, L.; Zelante  
Biochem. Biophys. Res. Commun. 250, 240-245, 1998  
A: Title: GABA (gamma-amino-butyric acid) neurotransmission: Identification and fine m  
A: Reference number: JE0356; MUID:98440782  
A: Accession: JE0356  
A: Molecule type: mRNA  
A: Residues: 1-960 <GRI>  
A: Cross-references: GB:Y11044; NID:g2826760  
A: Note: this ORF is not annotated in GenBank entry HSGTHLAL, release 109  
C: Genetics:  
A: Map position: 6p21.3-6p21.3  
C: Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein  
F: 1-960/Domain: signal sequence #status predicted <SIG>  
F: 12-960/Product: gamma-aminobutyric acid receptor B #status predicted <MAT>  
F: 590-613/Domain: transmembrane #status predicted <TM1>  
F: 627-654/Domain: transmembrane #status predicted <TM2>  
F: 666-687/Domain: transmembrane #status predicted <TM3>  
F: 709-730/Domain: transmembrane #status predicted <TM4>  
F: 767-788/Domain: transmembrane #status predicted <TM5>  
F: 803-825/Domain: transmembrane #status predicted <TM6>  
F: 831-856/Domain: transmembrane #status predicted <TM7>  
F: 23,83,439,481,501,513,630/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 46.3%; Score 2024.5; DB 2; Length 960;  
Best Local Similarity 49.4%; Pred. No. 1.8e-149;  
Matches 385; Conservative 151; Mismatches 220; Indels 23; Gaps 9;

QY 24 PHLQGGVAGRPDE--LHIGGIFPIAGKGWGGQACMPATRLALDDYKNPILPGFKLI 81  
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
Db 154 PHQVNRTPHSERRAVY1GALFPM--GGWPGGACQAPAVEMALDYNSRRDILPDYELK 211  
QY 82 LHSNDECEPGLGASVMYNNLYNKPQKMLLAGCSTVCTTVAAEAKMNNLIVLCYGASSP 141  
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :  
Db 212 LIHDSKCDPGQATKYLYELLYNDPIKILMPGCGSSYTLVAEARMNNLIVLSYGSSP 271  
QY 142 ALSDRRFPPLFTHPSTVHNPTRIKMKFGWSVAIIQQAAEEVISTVEDLENQME 201  
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
Db 272 ALSNRQFPFFRPHPSATLHNTRVKLFKRWGKKTKTTOOTTEVTSTUDDLEERVEK 331  
QY 202 AGVEITVRQSFSLDPTDAVRNLRQDARIIVGLFVYVAARRVLCENTYKQOYLGRAHWYFF 261  
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
Db 332 AGIEITFRQSFSDPAVPVKNLKRQDARIIVGLFYETEARKVFCVEYKERLFGKKYVWFL 391  
QY 262 IGWEDNWNVFNKAEQITCTVQMRITAEAGHLTTEALMNNQNTTISGTAEEFRHL 321

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Db 392 IGWYADNFEKI--YDPSINCTVDEMEFAVEGHITTEIVMLNPANTPANSISNWTSEFVEKL 449
QY 322 NOALIEEGYDINHRYPE---GYOEPAPLAYDAVMSVALAFNKNKMERLTTGKKSURDFTYT 378
Db 450 TKRL-----KRHEETGGFQEPAPLAYDAIWAALALANKTSGGGRSGVRLEDENYN 500
QY 379 DREIADIEAAMNSTOFLGSGVGVAFSSOGDRALTQIEQIDMGKYEKLGYDQDNLNLS 438
Db 501 NOTITDOIIRAMNSSBFGVSGHVFDASGRMAWTLIEQPQGSYKKGIGYDSTKDDLS 560
QY 439 WLNTQEWIGKVPQDRITIVHVLRTVSLPLFCVMCTISSCGIFVAFALIIIFNIWNKHRRV 498
Db 561 WSKTDKWIIGSPADQTLVLTFRFLSOKLFISVSVLSSGIVLAVVCLSFNIYNHVRV 620
QY 499 IOSSHVPVCNTIMLFGVIICLSVILGIDGRFVSPPEYPKICQARAWLLSTGFTLAYGAM 558
Db 621 IONSOPNLNLTAVGCSLAAAVPLGLDGYHIGRNQFPFVQCARLWLLGLGSLGYSM 680
QY 559 FSKVWRVHR-FTTK-AKTDPKKKVPEWKLYTMVSGLLSIDLVILLSQIIFDPLQRYLET 616
Db 681 FTKIMWVHTGFTKKEBKEKWKLTLPWKLYATVGLLVGMDVLTIAIWOIVDPLHRTIETF 740
QY 617 PLEDPVSTDDKIRPELEHCESSORNSMWLGVLVYGFKGLILVGLFLAYETRSIKVKOIN 676
Db 741 AKPEPKEDI-DVSLPQLEHCSRKNKNTWLGIFYGAGLLGLLGLFAYETKSVSTEKN 799
QY 677 DSRVYGMYSNVVLCITAPVGMVIAQQDASFAFVALAVIFCCFLMLLIFYPKPIEV 736
Db 800 DHRVAGMAYNVAVLCITAPVTMILSSQDAAFAFASLAIVFSSYITLVLVFVFKMRL 859
QY 737 IRHP--KDAESKYNPDSAISKEDEERYQKLVTEQQLRLITQKEKIRVLRORLVER 793
Db 860 ITRGEWQEAQDTMKTGSSNTNNEEKSRLLEKENRELEKIIAEKERVSELRLQLOS 918

RESULT 2
T29703
hypothetical protein ZK180.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
A:Accession: T29703
R:Pauley, A.; Le, T. T.
submitted to the EMBL Data Library, May 1996
A:Description: The sequence of C. elegans cosmid ZK180.
A:Reference number: Z20669
A:Accession: T29703
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-402 <PAU>
A:Cross-references: EMBL:U58748; PIDN:AA852965.1; GSPDB:GN00022; CESP:ZK180.1
A:Experimental source: strain Bristol N2; clone ZK180
C:Genetics:
A:Gene: CESP:ZK180.1
A:Map position: 4
A:introns: 25/3; 98/2; 219/3; 253/3; 280/1; 309/1; 339/2; 357/3; 395/2

Query Match 10.4%; Score 457; DB 2; Length 402;
Best Local Similarity 29.9%; Pred. No. 1e-27;
Matches 132; Conservative 74; Mismatches 161; Indels 74; Gaps 15;

QY 389 AMNSTOFLGSGVGVAFSSOGDRIALTQIEQIDMGKYEKLGYDQDNLNLSMLN--TEQWI 446
Db 15 AIDNSSFQGLTGKVKFAN-NERGLVDIKOWSDQYVFAVYDGDADDEKFIIDSTTKGW- 72
QY 447 GGVVPDQRTIVHVLRTVSLPLFCVMCTISSCGIFVAFALIIIFNIWNKHRRVIOSSHVPC 506
Db 73 --SPPLDSTITERRRHHISILFAM-----SLF-----IKMSSPNL 107
QY 507 NTIMLFGVICLSVILGIDGRFVSPPEYPKICQARAWLLSTGFTLAYGAMFSKVRVRVH 566
Db 108 NMLIIAGSICTFASVIMGLDTRIVSPDVFVWLCYTNWTLCIGFTLSFGAMFSKTRVRVH 167
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QY 567 RETTAKTDPKKKVPWKLYTMVSGLLSIDLVILLSQIIFDPLQRYLETFFLEDPVSTTD 626
Db 168 SIFTNIRM-D-RAAIRKDSKLFILGILLFIDICVLVTWAFVSPFS-YTVT---ELPHIPED 222
QY 627 DIKIRPELEHCESSORNSMWLGVLVYGFKGLILVGLFLAYETRSIKVKQINDSRVGMYSIY 686
Db 223 NIVIIPEVEKCNSSGSGVQAVLYAVKGVLMILGCFLAWETRHVNVPALNDSKIYIGTR-- 280
QY 687 NVVVLCLITAPVGMVIAQQDASFAFVALAVIFCCFL---SMLLIFVPKVIIEVIRHPKDK 743
Db 281 -----TGQRDVQSREV-----FCHFLDITNVVSRECAKDSKFSKTPNFI 319
QY 744 AESKNPDSAISKEDE---ERYOKLVTEQQLRLITQKEKIRVLRORLVERGDAGKE 800
Db 320 MKLFFN----FSKNSYGGFKNFQKLSFGGFNIVFARSOVKKKVIELARNPV-----GNE 369
QY 801 LNG-ATGVASAAVANTSOPAS 820
Db 370 PRAYRRGLMKSVVAKTSOPMS 390

RESULT 3
JH0563
metabotropic glutamate receptor 4 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 17-Nov-2000
A:Accession: JH0563; I58149
R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A:Title: A family of metabotropic glutamate receptors.
A:Reference number: JH0561; MUID:92110002
A:Accession: JH0563
A:Molecule type: mRNA
A:Residues: 1-912 <TAN>
A:Experimental source: brain
R:O'Hara, P.J.; Sheppard, P.O.; Thøgersen, H.; Venezia, D.; Haldeman, B.A.; McGrane,
Neuron 11, 41-52, 1993
A:Title: The ligand-binding domain in metabotropic glutamate receptors is related to
A:Reference number: I58149; MUID:93332699
A:Accession: I58149
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-123, 'R', 125-912 <RES>
A:Cross-references: GB:M90518; NID:g205400; PIDN:AAA93190.1; PID:g205401
C:Comment: This protein is coupled to a G protein and evokes a variety of functions
C:Genetics:
A:Gene: GLUR4
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phos
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-912/Product: metabotropic glutamate receptor 4 #status predicted <MET>
F:588-610/Domain: transmembrane #status predicted <TRI>
F:625-645/Domain: transmembrane #status predicted <TII>
F:657-675/Domain: transmembrane #status predicted <TII>
F:700-720/Domain: transmembrane #status predicted <TIV>
F:751-772/Domain: transmembrane #status predicted <TRV>
F:786-807/Domain: transmembrane #status predicted <TVI>
F:822-847/Domain: transmembrane #status predicted <VII>
F:98,301,454,484,569/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:621,689,695,859,870/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 8.2%; Score 356.5; DB 2; Length 912;
Best Local Similarity 18.9%; Pred. No. 2.5e-19;
Matches 177; Conservative 164; Mismatches 374; Indels 221; Gaps 36;

QY 5 MTSQDGAFTFW--IFLLCLIAS-----PHLQGVAGRP-----DELHIGGIFFIAGK 48
Db 1 MSCKGGMWAWRLPLCLLLLSLYAPVWPSSLGPKPKPHMNSIRIDGDTLGLGLFPVHGR 60
QY 49 GWOQGOAC-----MPATRLALDDVKNQPNLLPFGKIL----- 80
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Db 96 LDTCSRDTYALEQSLFVRASLTAKVDAEYMCPLDG-----SYATQENIP-----LLIAGVIG 147

QY 116 ----STVCTTVAEAKMNLIVLCYGASSPALSDRKRPTLFRTHPSATVHNPTRIKLMKK 172

Db 148 GSYSSVSIOVALLRLFOIQISVASTSAKLSDSRVDYFARTVPPDFYQAKAMAEILRY 207

QY 173 FGRSRVAILQQAEEVFISTVEDLE-----NRCMEAGVEIVTROSFLSDPTDAVRN-LRR 225

Db 208 FNTYVSTVASEGDYGETGEAFQEAEARLNICIT-ATAEKVGRSNIRKSYDSVIRELQK 266

QY 226 QDARIIVGLF-----YVVAARVLCEMYKQOLYGRAHWFFIGTWEDNMYEVLKAE 277

Db 267 PNARVV-LFWRSDSRELIAASRV-----NASFTWV-----ASDQWG-----AQE 307

QY 278 GITCTVEQMRIAABGLHTTEAL-----MNQNNQTTIS 310

Db 308 SI---VKGSEHVAIGAITLELASHPVRFQDRYFOSLNPYNNHNPWFDFWEQFQCSLQ 364

QY 311 GMTAEFRHLNQAIEEGYDINHIDRYPEGYQAEPLAY--DAVWSVALAFNKTWERL--- 365

Db 365 -----NKRNRHQICDKHLAIDSSNYE---QESKIMFVNNAVYAMAHALHKMORTLCPN 414

QY 366 TT-----GKKSRLRDTYTTDKETADEIYAAMNSTQFLGVSQVAFSSQGDRIALTQ 415

Db 415 TTLCDDAMKILDKKKLYKDYL-----LKNFTAPFNPK--GADSIKVFDTYDGMGRYN 467

QY 416 I--EQMIDGRYE--KLGYDTQL-----DNLSQLNTE----- 443

Db 468 VFNFQHIGGKSYLKVGHWAEATLYLDVDSIHSRSNVSPTSCSDPCAPNEMKNQPGDVC 527

QY 444 -----QW-----IGG--KVPQDRTIVTHVL 462

Db 528 CWICICEPEYELVDEFTCMDCGPGQWPTADLSGCYNLPED-----YIRWEDAWAIGPV 581

QY 463 TVSLPLFVCMCTISSCGIFAFALIIENIWNKRR--VQSSHPVCMNTIMLFGVIICLI 519

Db 582 TIACLGFMCTC-----IVTVFKHNNTPLVKASGRELC-YILLFGVLSYC 627

QY 520 SVILLGIDGRFVSPEEYKPKICQARAWLLSTGFTLAYGAMFSKVRVHRTTKAKTDPK-- 577

Db 628 MTF-----FFTAQSPVICALRRRLGLTSGFAICY SALLTKTNCIARIFDGVNGAQR 680

QY 578 KVEPKMLYPMVSGLLSIDVLLSWQIFDP--LQRYLETFFLEDVSTTDDIKIRPELE 635

Db 681 KFTSPSQVFICLLILVQVWVSWLILETPGTRRY--TLP-----EKRETVIL 728

QY 636 HCSQRNSMWGLVYGFGLILVGLFLAYETRSIKVKQINDSRVGMYSIYVNVVLCIT 695

Db 729 KCVKQSSMLISLYDY--VLVILCTVYAFKTRKCP-ENFNEAKFIGHTMTYTTCIIWLAF 785

QY 696 APVGMVITASQODASFAFVALAVIFCCFLSMILLIFVPKVIEWIRHPK 741

Db 786 LPFIYVTSYRQVQTTTMCISVLSGFEVLGCLFAPKPVHVLFPQ 831

## RESULT 7

A46742  
metabotropic glutamate receptor, mGluR6 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Jun-2000  
C:Accession: A46742  
R:Nakajima, Y.; Iwakabe, H.; Akazawa, C.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, J. Biol. Chem. 268, 11868-11873, 1993  
A:Title: Molecular characterization of a novel retinal metabotropic glutamate receptor mGluR6  
A:Reference number: A46742; MUID:93280152  
A:Accession: A46742  
A>Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-871 <NAK>  
A:Cross-references: GB:D13963; NID:G91856; PIDN:BAA03066.1; PID:g931857  
A:Experimental source: retina  
A>Note: sequence extracted from NCBI backbone (NCBIN:133246, NCBI:P.133250)  
C:Superfamily: metabotropic glutamate receptor 4

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 7.6%; Score 334.5; DB 2; Length 871;  
Best Local Similarity 20.3%; Pred. No. 1.2e-17;

Matches 180; Conservative 158; Mismatches 350; Indels 199; Gaps 39;

QY 11 VTFWTF---LLCLIASPHLQGGVAGRPDEHLHIGGIFPIAGKGGWQGCAC----- 57

Db 11 LAWLWSQAGIACGAGSVRLAGG-----LTGLGLFPVHARGA--AGRACGALKKEQGVH 61

QY 58 -MPATRLALDDVKNQPNLLPGFKLILHNSDSECE-----PGLGA 95

Db 62 RLEAMLYALDRYADNPPELLPGVRLGARLLDT-CSDRTYALEQALSFEQALIRGRGDGEA 120

QY 96 SV-----MYNLLYNPKOKLMLLAG--CSTVCTTVAEAAKMWNLIVLCYGASSPALSDRKR 148

Db 121 SVRCGGVPPLSAPSERPVAVVGASSVSMVANVLRFAIPQISYASTAPELSDSTR 180

QY 149 FPTLFRTHPSATVHNPTRIKLMKKFGSRVAIL-----QQAEEVFISTVEDLENRCME 201

Db 181 YDFFSRVVPDPSYQAQAWDIVRALGWNVYSTLASSENGYSGEVEAFQISREAGGVCTA 240

QY 202 AGVEIVTROSFLSDPTDAVRNLR--ODARILVGLFYVVAARRVLCEMYKQOLYGRAH 257

Db 241 QSIKIPREPCK---PGEFHKVIRRLMETPNAGIILIFANEDDIRRVELEATROANLTGH-- 294

QY 258 VWFEGTGWEDNWE-----VNLKAEGI-TCTVEQMRIAAG---HLTTEALMNQNNQTT 308

Db 295 -FLWVG--SDSWGSKISPIILNLEEEAVGAILPLPKRASIDGFDQYFMTFSL---ENNRN 348

QY 309 TSGMTAEFRHLNQAIEEGYD-----INHIDRYPEGYQAEPLAYDAVWSVA 355

Db 349 I--WFAEWEENFNCKLTSSGGQSDSTRTKCTGEEIGODSAYEQEGKVFQVIDAYATA 406

QY 356 LAFNKTMERLTTGKSL-RDFTYTKDEIADEIYAAMNSTQFLGVSQV--VAFSSQGD---R 410

Db 407 HALSHMQALCPGHTGLCPAMEPTD--GRTLLHYIRAVRFNGSACTPVMEENGADAPGR 463

QY 411 TALTOIE-----QMDGKYEKLGYY--DTOLDNLWSLNTQEWIGG--KVPQDRTIV----- 457

Db 464 YDIFYQATNGSSASSGGYQAVGQWAEALRLD---MEVLWSDGDPHEVPPSCSLPCGPG 519

QY 458 -----THVLR-TVSLPL 468

Db 520 ERKMKVGPCCWHCEACDGYRFQVDEFTCEACPGDMRPTPHNHTGCRPTPVVRLTWSSPW 579

QY 469 FVCMCTISSCGIFAFALIIENIWNKRRVSIQSSHPVCNTIMLFGV-IICLSVILLGID 527

Db 580 AALPLLLAVLGIMATTTIMATFMRHNDTPIVRASGRELSVLLTGIFLIYATFLMVA-- 637

QY 528 GRFVSPEEYKPKICQARAWLLSTGFTLAYGAMFSKVRVHRTTKAK--TDPKKKVEPKL 585

Db 638 -----EPCAAICAARRLLILGLTTLISYALLTKTNIYRIFEQGRSVTPPPFISPTSQ 691

QY 586 YTMVSGLLSIDVLLSWQIFDPLQRYLETFFLEDVSTTDDIKIRPELEHESQRNSMW 645

Db 692 LVITFGLTSLQVGVIAWLGAPPHSVID-----YEQRTVDEQARGVLK-CDMSDLSL- 745

QY 646 LGLVYGFGLIILVGLFLAYETRSIKVKQINDSRVGMYSIYVNVVLCITAPVGMVIAQ 705

Db 746 IGCL-GYSLLLMVTCTVVAIKARGVP-EFNEAKPIGFTMYTTCIIWLAFVPI--FFGTA 801

QY 706 QDASFAFY-----ALAVIFCCFLSMILLIFVPKVIEWIRHPKDKAESK 747

Db 802 QSAEKIYIQTTLTVSLSLASVSLGMLVVPKTVYILPHPEQNVQKR 848

## RESULT 8

JH0562  
metabotropic glutamate receptor 3 precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 13-Sep-1998

C;Accession: JH0562  
R;Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.

Neuron 8, 169-179, 1992

A;Title: A family of metabotropic glutamate receptors.

C;Date: 30-Jun-1992 #sequence #status predicted <SIG>

C;Accession: JH0561; MUID:92110002

A;Molecule type: mRNA

A;Residues: 1-879 <TAN>

A;Experimental source: brain

C;Comment: This protein is coupled to a G protein and evokes a variety of functions by

C;Superfamily: metabotropic glutamate receptor 4

C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-879/Product: metabotropic glutamate receptor 3 #status predicted <MET>

F:577-599/Domain: transmembrane #status predicted <TRI>

F:614-634/Domain: transmembrane #status predicted <TII>

F:646-664/Domain: transmembrane #status predicted <III>

F:689-709/Domain: transmembrane #status predicted <TIV>

F:735-756/Domain: transmembrane #status predicted <TRV>

F:770-791/Domain: transmembrane #status predicted <TVI>

F:804-828/Domain: transmembrane #status predicted <VII>

F:209,292,414,439/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:610,845/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 7.6%; Score 333; DB 2; Length 879;

Best Local Similarity 20.6%; Pred. No. 1.6e-17;

Matches 180; Conservative 132; Mismatches 313; Indels 250; Gaps 39;

QY 36 ELHIGGIPIACKGGWGGQAC-----MPATRLALDDVKNOPNLLPGFKLLHS 84

Db 38 DLVLGGLFPINEKG--TGTECGRINEDRGIOKLEAMLFADINDKNYLLPGVKLGVIH 95

QY 85 NDS-----ECEPGLGASVMYLLYNKKPKMLLAGC-- 115

Db 96 LDTCSRDYALQSLLEFVRASLTKVDEAYMCPDG-----SYAIQENIP---LLIAGVIG 147

QY 116 ---STVCTTVABAAKMNNLIVCYGASSPALSRRKRPFTLFRPHSATVHNPTRIKLMKK 172

Db 148 GSYSSVSIQVANLLRFQIPQISYASTSAKLSKSDYDFARTVPDPYQAKAMAEILRF 207

QY 173 FGMSRVAILOQAEVFIISVEDE-----NRCMEAGVELVTRQSLDPTDAVRN-LRR 225

Db 208 FNMVTSTVASGDEYGETGIEFAEQEARLNICI-ATAEKVGRNSRKSYSVIRELLQK 266

QY 226 QDARIIVGLF-----YVVAARRVLCEMYKQOLYGRAHVWFIFGWYEDNNYEVNLAKE 277

Db 267 PNARVVV-LFMRSDDSRELIANRV-----NASFTWV---ASDCWG-----AQE 307

QY 278 GITCTVEQMRIAEGHLLTTEAL-----MWNQNNQTTIS 310

Db 308 SI---VKGSEHVAYGAITLASHPVQRDQRYFQSLNPNYNNHRNPWFRDFWEQKFCQSLQ 364

QY 311 GMTAEFRHLQAILEEGYDINHDPYEGYQEAPLAY--DAVSVALAFNKWTHERLTG 368

Db 365 -----NKRNRHQVCDKHLADSSNYE---QESKTFMVVNAVYAMALHMKQRTLCPN 414

QY 369 KKSRLF--TYTDKEIADIEYAMNNTQFL---GSGVVVAFSSQGDRIALTQI--EOMI 420

Db 415 TTKLCDAMKILDGKKLYKEYLLKINTAPNPNKGADSIKFTDFDGMGRYVNFNLQQT 474

QY 421 DGKYE--KLGY--DTQLDNLW---INTEQ-----WI----- 446

Db 475 GKKSYLVKGHWAETLSLDVDSIHWRSNVSPTSQSDPCAPNEMKNMQPGDCCWICIPC 534

QY 447 -----GGKVP-----QDRTTVTHVLRVSVPLFCVCMC 473

Db 535 EPEYELVDEFTCDGPGQMPADLSGCYNLPEDYIKWEDAWAIGPV--TIACGLFCTC 592

QY 474 TISSCGIFAFALIFNIWKKRR---VIQSSHPVNTMLFGVILCLISVILLGIDGRF 530

Db 593 -----IVTTFIKHNNTPLVKSAGRELK-YILLFGVSYSUCMTF-----F 631

QY 531 VSPEEYKICQARAWLLSTGFTLAYGAMFSKVMVHRHTTKAKTDPK--KKVEPKLYTM 588

Db 632 FIARQSPVICALRLGLGTSFAICYSALLTKTNCIARIDGKNGAQRKFISSQVFI 691

QY 589 VSGLLSDLVILLISQWIFDP--LQRYLETFFLEDVSTDDIKIRPELEHESQNSMWL 646

Db 692 CLGILILQIVMVSWMILLETPTGTRY--TLP-----EKRETVILKCNVRDSSMLI 739

QY 647 GLVYFGKGLILVFLGLFLAYETRSIKVKQINDSRVYVMSIYNNVVLCLITAPVGMVIAQQ 706

Db 740 SLATYDV--VLVILCTVYAFNTRKCP-ENFNEAKFIGFTMYTTCIILWLAFLFIYVTSDDY 796

QY 707 DASFAFVALAVICCFSLMLLIFVPKVIEWIRHPK 741

Db 797 RVQTTTMCISVLSGFFVVLGCLFAPKVIHILFQPO 831

RESULT 9

JH0561

metabotropic glutamate receptor 2 precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Jun-1992 #sequence #status predicted <SIG>

C;Accession: JH0561

R;Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.

Neuron 8, 169-179, 1992

A;Title: A family of metabotropic glutamate receptors.

C;Reference number: JH0561; MUID:92110002

A;Accession: JH0561

A;Molecule type: mRNA

A;Residues: 1-872 <TAN>

A;Experimental source: brain

C;Comment: This protein is coupled to a G protein and evokes a variety of functions b

C;Superfamily: metabotropic glutamate receptor 4

C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-872/Product: metabotropic glutamate receptor 2 #status predicted <MET>

F:568-590/Domain: transmembrane #status predicted <TRI>

F:605-625/Domain: transmembrane #status predicted <TII>

F:637-655/Domain: transmembrane #status predicted <III>

F:680-700/Domain: transmembrane #status predicted <TIV>

F:726-747/Domain: transmembrane #status predicted <TRV>

F:761-782/Domain: transmembrane #status predicted <TVI>

F:795-819/Domain: transmembrane #status predicted <VII>

F:203,286,338,402,547/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:601,675,827,837,843/Binding site: phosphate (Ser) (covalent) #status predicted

F:832/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 7.3%; Score 318; DB 2; Length 872;

Best Local Similarity 19.7%; Pred. No. 2.4e-16;

Matches 181; Conservative 135; Mismatches 330; Indels 274; Gaps 38;

QY 17 LLCLIASPHLOGGVAGRP-----DELHIGGIFPIAGKGGWGGQACMP----- 59

Db 4 LLGLFALLLLMGVAEGPAPKVLTLGLDLVLGLFPVHQKGG--PAEECGPVNEHRTQ 61

QY 60 --ATRLALDDVKNOPNLLPGFKLLHSNDS-----EC 89

Db 62 LEAMLFALDRINRDPHLLPGVRLGAHLILDSCKDTHALEQALDFVRASLRGADSRHIC 121

QY 90 EPGLGASVMYNNLKNPKQLMLLAG--CSTVCTTVABAAKMNNLIVCYGASSPALSQRK 147

Db 122 PDG-----SYATHSDAPTAVTGVIGGYSVDSIQVANLLRFLFQIPQISYASTSAKLSDKS 176

QY 148 RPTFLRTHPSATVHNPTRIKLMKKFGHSRVAIL-----QQAEEVVIS 190

Db 177 RYDYFARTVPDPDFQAKAMAEILFRFNNTYVSTVASGDEYGETGIEFAELEARANICVA 236

QY 191 TVELENRCMEAGVEIVTQSFSLDPTDAVRN--RRDARILVGLFVVAARRVLCEMY 248

Db 237 TSEKVGAMSRARAEQGVVR-ALLQKPSARVAVLFRSEDAREL-----LAATQRL----- 285

QY 249 KQOLYGRAHVWFFIGWYEDNNYEVNLAKEGICTCTVEQMRIAEGHLLTTEALM----- 300

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Db 286 -----NASFTW-----ASDGHGAL-----ESVVGASER---AAEGAITIELASYPISDFAS 329
QY 301 -----WNQNOTTISGMTAEFR-----HRLNQALIEBQYDINHRYPEGYQE 343
Db 330 YFQSLDPWNSRNPFREFWEERHCSFRQDCAHSLRAVPFE-----QE 375
QY 344 APLAY---DAVWSVALAFNKMTWRL-----TTGKSLRDFYTDK-----380
Db 376 SKIMFVNNAVYAMAHALHMHRLCPNTHLCDAMPVNGRRLYKDFVLNKFDAFFRPA 435
QY 381 EIADIEIYAAMNSTOFLGSGVVAFFSSQDRIALTOIEQWIDG-----KYEKLGYY-----430
Db 436 DTDDE-----VREDFGDIGRYNIFYLRAGSGRYRQKVGWBAEGLT 479
QY 431 -DTQDLNLSWLNTBQWIGGKVPQDR---TIVTHVRLVSLPLFVC---MC-----473
Db 480 LDTSF---IPWASPS---AGPLPASRCSEPCLONEKVSQV-PGEVCCWLCIPQPYEYRLD 533
QY 474 -TISCGI-----FVAF-----ALIFINWKNHR 496
Db 534 EFTCADCGLYGWPNASLTGCFELPOEYIRWGDAMAVGPVTIACLGALATFLVGLVFEVRHN 593
QY 497 R-VIQSHHPVCNTIMLFGVILICLSVLLIGIDGRFVSPPEYKPKICQARAWLLSTGFTLA 554
Db 594 ATPVVKASGRELCYILGGVFLCYCMTFV-----FIA-KPSTAVCTLRRLGLGTAFSVC 646
QY 555 YGAMFSKVRVHRTTAKTDPKKK---VEPWKLYTWVSGLLSIDAVILLSHQWIFDPLQRY 612
Db 647 YSALLTNTNRITARIFGAREGAQRPFISPASQVAICLALISQGLLIIVAAMLVVEAPGTG 706
QY 613 LETPLEDPVSTDDIKIRPELEHCEQSQRNSMWLGVLVYGFGLIILVFLGFLAYETRSIKV 672
Db 707 KETAPERREVTL-----RCNHRDASMLGSLAVNV--LLIALCTLYAFKTRKCP- 753
QY 673 KQINDSRVYVGSYINVVVLCLITAPGVMIASQDASFAFVALAVIFCCFLSMLLIFVPK 732
Db 754 ENFNEARFIFGFTMTTCIILWLAFLPIFYVTSDDYRVQTTMCVSVSLSGSVVLGCLFAPK 813
QY 733 VIEWIRHPKDAESKYNPDS 752
Db 814 LHIILOFOKNVWVSHRAPTS 833

RESULT 10
A42916
metabotropic glutamate receptor mGluR5 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A42916
R:Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
J. Biol. Chem. 267, 13361-13368, 1992
A:Title: Molecular characterization of a novel metabotropic glutamate receptor mGluR5
A:Reference number: A42916; MUID: 92317054
A:Accession: A42916
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1171 <ABE>
A:Cross-references: GB:dl0891; NID:g220813; PIDN:BAA01711.1; PID:dl002186; PID:g220814
A:Experimental source: brain
A>Note: sequence extracted from NCBI backbone (NCBIN:107749, NCBIPI:107750)
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 6.9%; Score 303.5; DB 2; Length 1171;
Best Local Similarity 19.9%; Pred. No. 5.1e-15;
Matches 203; Conservative 144; Mismatches 387; Indels 287; Gaps 43;

QY 30 VAGRPDELHGGTIPPI-----ACKGQWQGGQACMPATRLALDDVKNQPNLLP 76
Db 28 VAHMPGDIILGALFSVHHQPTVDKVRHCKGAVREQYGIQRVTEAMLHTLERINSPTLLP 87
QY 77 GFKLILHSND-----SECEPCL-----GASVWYNLLYNKPKQL 109
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Db 88 NITLGCIEIRDSCWHSVAVALEQSIETIRDSLSISEEEGLVRCVDGSS---SFRSKKPIVG 144
QY 110 MLIAGCSTVCTTVAEAAKMNLLVLCYGASSPALSORKRPTTLFRTHPSATVHNPTRIKL 169
Db 145 VIGPGSSVAIQVONLLQLENIPQIAYSATSMDSLTKLFKPMRVVPSDAQARAWDI 204
QY 170 MKKFGNSRVAILOQAAEEVFISTVEDLENRCMEAGVEIVTRQSFLSDPTD-----AVNLR 224
Db 205 VKRYNNTYVSAVHTEGNYGESGMEAFKMSAKEGICIAHSYKIYSNAGEOSFKLLKLR 264
QY 225 RQ---DARIIVGLFVYVAARVCLCENKQOILYGRAHWWFFIGWTEDNW---YEV-----NL 274
Db 265 SHLPKARVACFCGEGTVRGLMAMRRLGLAGE-----FLLLSGDGWADRYDVTGYQRE 319
QY 275 KAEGICTCTVEQ-----MRIAAEGHLLTEAL--MWNQNOTTISGMTAE--EPRHR 320
Db 320 AVGGITIKQSPDKVDFDDYYLKLRPETNLNRFWFQHFQHRFCQCRLEGPAQENSKYNT 379
QY 321 LNQALIEGYDINHRYPEGYQAPLAY---DAYMSVALAFNKMTWRLTTGKSLRDFYTT 378
Db 380 CNSSLTLRTHV-----QDSKMGFVINAISYMAAYGLHNMQMSLCPGYAGLCD--A 427
QY 379 DKEI-ADEIYAAMNSTOFLGVSG-VVAFSSQGDRIALTOIEQWIDGKYEKLYGYDQLDN 436
Db 428 MKPIDGRKLIDLSLTKNTFTGVSGDMILFDENGDS-----PGRYEIMNEKMGKDY 477
QY 437 LSWLNTAEQWIGKVPQDRITV---THVLRTV-SLPL-----468
Db 478 FDIYINGVNDGELKWDDEWMSKNNIIRKSVCEPCEKQIKVIRKGEVSCCWTCTPK 537
QY 469 -----FVC-MCTISS-----CGIF-----VAFAL 486
Db 538 ENEYVFEDEYCKACQIGSNWPTDDLTCGLIPVOYLKWDPEPIAAVAVFACLLGLLAVT 597
QY 487 IIFNIWKNHRRVIOSSHHPVCNTIMLFGVII-----CLISVILLIGIDGRFVSPPEYKIC 540
Db 598 VIFIIYRDTFVVKSSSREL-C-YIILAGICLGLYLCFCLIA-----KPK-- 639
QY 541 QARAWLLSTGF-----TLAYGAMFSKVRVHRTTAKTDPKKVEPWKLYTWVSGLLSID 596
Db 640 QIYCYLQRIIGIGLSPAMSYSALVTKTNRILAGS-----KKKICKKPRFMSACQLVI 695
QY 597 LVILLSQWIFDPLQRYLETFFLEDPVSTDDIKIRPELEHCEQSQRNSMWLGVL--YGFKG 654
Db 696 AFILICIQ---LGIIVALFIMEPPDIMHDYPSIREVYLIC-----NTNLGVVTPGLYNG 747
QY 655 LILVGLFLAYETRSIKVKQINDSRVYVGSYINVVVLCLITAPGVMIASQDASFAFVA 714
Db 748 LLILSCTFFYAFKTRNYP-A-NFNEAKYIAFTMTYTCIILWLAFFVI-----YFGSN 795
QY 715 LAVIFCCF-----LSMLLIFVPKVIETIRHPKDAESKYNPDSAI-----SKEDE 799
Db 796 YKIITMCFVSLSATVALGCMFVPKVIILAKPERNVRSFTTSTVVRMHVGDGKSSAA 855
QY 760 ERYQKLV-----TENEQ-----LQRL---ITQKEK-----782
Db 856 SRSSLSLVNLWKRSGSGETLSSNGSKVSWAONEKSTRGHLMWRLSVHINKKENPOTAV 915
QY 783 IIVLRQLRVERGD---AKTELGATGAVASAAVATTSQPASLINNSAHATPAATLAIOTG 839
Db 916 IKFPFKSTENRGGAAGSGGPGVAGAGNAGCTATGCP-----EPPDAGPKALYDVAEA 970
QY 840 E 840
Db 971 E 971

RESULT 11
S71376
glutamate receptor homolog - cherry salmon
C:Species: Oncorhynchus masou (cherry salmon)
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 01-May-1998
```



Db 425 LCD---AMKPIDGRKLLBSLTKNTGYSGDTILFDENGDS-----PGRYEIMNF 471  
QY 430 YDTQDNLNLSWLNTEOMIGKVPQDRIV---THVLRTV-SLPL----- 468  
Db 472 KEMGKDYFDYINVGSWDNGELKMDDEWVSKSNIIRSVCEPKGQIKVIRKGEVSC 531  
QY 469 -----FVC-MCTISS-----CGIF----- 481  
Db 532 WTCPCKENEYVDEYTCACQGLGSMPTDGLTGCDDLPVQYLWGDPEPIAAVVFACGL 591  
QY 482 --VAFALIIFNWKNHRRVIOSSHPVCNTIMLFGVII-----CLISVILLGIDGRFVSP 533  
Db 592 LATLFVTVFIYRDTPVVKSSREL-C-YIILAGICLGLYCTFCLIA----- 637  
QY 534 EEPKICQARAWLLSTGF---TLAYGAMFSKVMVRHRTTKAKTDPPKKVPEPKLYTMV 589  
Db 638 --KPK--QIYCYLQRIQIGLSPAMYSALVTKTNRIARLAGS-----KKKICTKPRFMS 689  
QY 590 SGLLSIDLVLISWQIFDPLQRYLETFPLEDPVSTDDIKIRPELEHCEQSQRNSMWGLV 649  
Db 690 ACAQLVIAFLICIQ---LGIIVAFIMEPPDMDHDPYSIREVYLIC---NTTNLGVV 741  
QY 650 --YGFKGLIIVFGLFLAYETRSIKVQINDSRVYVCMYSINNVVLCILITAPVGMVIAQQD 707  
Db 742 TPLGYNGLLILSCTFYAFKTRNPA-NFNEAKYIAFTMTTCIILWLAFFVI----- 791  
QY 708 ASFAFVALAVIFCCF-----LSMLLIFVPKVIIEVIRHPDKAKSKYNPDSAI----- 754  
Db 792 --YFGSNYKIITMCFVSLSATVALGCMFVKYIILAKPERNVSFAFTTSTVVRMHVGD 849  
QY 755 --SKDEERYOKLV-----TNEQ-----LQRL-----ITQKE 780  
Db 850 GKSSSAASRSSSLNWLKRRSGSGETLRSNGKSVTWQAQNEKSSRGHLWQLSIHINKKE 909  
QY 781 EKIRVLQRLVERGDAKTELN-----CATGVASAAVATTSOPASLINS 825  
Db 910 NP-----NQTAVIKFPFKSTESRGLGPRGAGSGAGVGTAGCAGAGPGGP-----ES 960  
QY 826 AHATPAATLAITQGE 840  
Db 961 PDAGPKALYDVAEAE 975

## RESULT 13

JC2131

metabotropic glutamate receptor 5 B - human

C:Species: Homo sapiens (man)

C&gt;Date: 28-Aug-1995 #sequence\_revision 07-Oct-1994 #text\_change 05-Jan-1996

C:Accession: JC2131

R:Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.

Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994

A:title: Molecular cloning and the functional expression of two isoforms of human metabo

A:Reference number: JC2131; MUID:94197696

A:Accession: JC2131

A:Molecule type: mRNA

A:Residues: 1-1212 &lt;MIN&gt;

C:Comment: This protein is coupled to guanine nucleotide binding proteins.

C:Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein

F;580-604/Domain: transmembrane #status predicted &lt;TM1&gt;

F;617-637/Domain: transmembrane #status predicted &lt;TM2&gt;

F;644-664/Domain: transmembrane #status predicted &lt;TM3&gt;

F;694-714/Domain: transmembrane #status predicted &lt;TM4&gt;

F;738-759/Domain: transmembrane #status predicted &lt;TM5&gt;

F;773-794/Domain: transmembrane #status predicted &lt;TM6&gt;

F;803-827/Domain: transmembrane #status predicted &lt;TM7&gt;

## Query Match

Best Local Similarity 6.8%; Score 297.5; DB 2; Length 1212;

Matches 194; Conservative 141; Mismatches 360; Indels 275; Gaps 41;

QY 30 VAGRPDELHIGGIPPI-----AGKGGWGGQACMPATRLALDDVWKNOPNLLP 76

||| : : : ||| : : ||| : : ||| : : ||| : : ||| : : ||| : : |||

## RESULT 14

T27628

hypotheetical protein 2c506.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C&gt;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000

C:Accession: T27628

Db 28 VAHMPGDIIGALFSVHHQFTVDKVERKCGAVREQYGIQVREAMLHLEIRNSDPTLLP 87  
QY 77 GFKLIHLSND-----SECEPL-----GASVMYNLLYNKPKQL 109  
Db 88 NITLGEIRDSCWHSVALEQSTIEFIRDSLSSEEEGLVRCVDGSSSFR--SKKPIVG 145  
QY 110 MLAGGSTVCTTVAERAKMNLLIVCYGASSPALSDRRKPTTLFRTHPSTVHNPTRIKL 169  
Db 146 VIGGSSSSVAIQVNLQILFNIPQIAYSATSMDSKTLFKYFMRVVPSDAQARAMVDI 205  
QY 170 MKFGFSRVAILOQAAEEVFISTVEDLENRCMEAGVEITVTRQSLSDPTD-----AVNLR 224  
Db 206 VKRYNTYVSATVTEGNYGESMEAFKMSAKEGICIAHSYKIIYSAGEQSFDKLLKLLT 265  
QY 225 RQ--DARIIVGLFVVAARRVLCMKYKQOQLYGRAHVFFIGWTYEDNW---YEV-----NL 274  
Db 266 SHLPKARVACFEGMTVRGLLMMRRLGLAGE-----FLLGSDGWADRYDVTGQYRE 320  
QY 275 KAEGITCTVBQ-----MRIAEGHLLTTEALMNNQNTTISGMTAEERFHLNQ 324  
Db 321 AVGGITIKLQSPDVKNFDDYILKRPB---TNHRNPWFQ-----EFQHRFQCR 366  
QY 325 LIEEGYDINHRY-----PEGYQAPLAY--DAVSVVALAPNKTMRERLTTGKKS 371  
Db 367 L--EGFPQENSKYKNTCNSSLTLKTHHVQDSKMGFVINALYSMAIYGLHNNQMSILCPGYAG 424  
QY 372 LRDTYTDKEI-ADEIYAAAMNSQFLGVSG-VVAFSSQGDRIALTOIEQMDCKYKELGY 429  
Db 425 LCD---AMKPIDGRKLLBSLTKNTGYSGDTILFDENGDS-----PGRYEIMNF 471  
QY 430 YDTQDNLNLSWLNTEOMIGKVPQDRIV---THVLRTV-SLPL----- 468  
Db 472 KEMGKDYFDYINVGSWDNGELKMDDEWVSKSNIIRSVCEPKGQIKVIRKGEVSC 531  
QY 469 -----FVC-MCTISS-----CGIF----- 481  
Db 532 WTCPCKENEYVDEYTCACQGLGSMPTDGLTGCDDLPVQYLWGDPEPIAAVVFACGL 591  
QY 482 --VAFALIIFNWKNHRRVIOSSHPVCNTIMLFGVII-----CLISVILLGIDGRFVSP 533  
Db 592 LATLFVTVFIYRDTPVVKSSREL-C-YIILAGICLGLYCTFCLIA----- 637  
QY 534 EEPKICQARAWLLSTGF---TLAYGAMFSKVMVRHRTTKAKTDPPKKVPEPKLYTMV 589  
Db 638 --KPK--QIYCYLQRIQIGLSPAMYSALVTKTNRIARLAGS-----KKKICTKPRFMS 689  
QY 590 SGLLSIDLVLISWQIFDPLQRYLETFPLEDPVSTDDIKIRPELEHCEQSQRNSMWGLV 649  
Db 690 ACAQLVIAFLICIQ---LGIIVAFIMEPPDMDHDPYSIREVYLIC---NTTNLGVV 741  
QY 650 --YGFKGLIIVFGLFLAYETRSIKVQINDSRVYVCMYSINNVVLCILITAPVGMVIAQQD 707  
Db 742 TPLGYNGLLILSCTFYAFKTRNPA-NFNEAKYIAFTMTTCIILWLAFFVI----- 791  
QY 708 ASFAFVALAVIFCCF-----LSMLLIFVPKVIIEVIRHPDKAKSKYNPDSAI----- 754  
Db 792 --YFGSNYKIITMCFVSLSATVALGCMFVKYIILAKPERNVSFAFTTSTVVRMHVGD 849  
QY 755 --SKDEERYOKLV-----TNEQ-----LQRL-----ITQKE 801  
Db 850 GKSSSAASRSSSLNWLKRRSGSGETLRSNGKSVTWQAQNEKSSRGHLWQLSIHINKKE 900  
QY 802 NGATGVASAA 811  
Db 901 NGGRATMSSS 910



Db	817	WRH--HYPTRDQVYLT-----CNVPDHHFLYSLAY--DGFLVILCTTYAVKTRK	861
QY	670	IKVKQINDSRVYGMISYNNVVLCLITAPGVMTASQODASFAFVALAVIFCCFLSMILLIF	729
Db	862	VP-ENFNETKTFIGFSMYTTCVWLWSWIFFFGTGSDFQIQTSISICISMSANVALACIF	920
QY	730	VPK--VIEVIRHP--KDKAESKNPDS-----AISKEDEERYOKLTVENEOLQ	773
Db	921	SPKLWILFLEKHKVNRQEGESMLNKSRSILGNCSRLCANSIDEPNOYTALLTDSTR--	978
QY	774	RLITQKEEKIRVLQRRLVERGDAGTELNGATGVASAAVATTQSPASLINSSAHAT	829
Db	979	-----RRSRK-----TSQPSF--TSSAHT	997

```

RESULT 15
A41939
G protein-coupled glutamate receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A41939; S15362
R:Houamed, K.M.; Kujper, J.L.; Gilbert, T.L.; Haideman, B.A.; O'Hara, P.J.
Science 252, 1318-1321, 1991
A:Title: Cloning, expression, and gene structure of a G protein-coupled g1
A:Reference number: A41939; MUID:92022526
A:Accession: A41939
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-1199 <HOU>
A:Cross-references: GB:M61099; NID:g397806; PIDN:AAA19497.1; PID:g204460
A:Experimental source: cerebellum
A:Note: sequence extracted from NCBI backbone (NCBIP:60785)
R:Masu, M.; Tanabe, Y.; Tsuhida, K.; Shigemoto, R.; Nakanishi, S.
Nature 349, 760-765, 1991
A:Title: Sequence and expression of a metabotropic glutamate receptor.
A:Reference number: S15362; MUID:91156047
A:Accession: S15362
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1199 <MAS>
A:Cross-references: EMBL:X57569; NID:g56646; PIDN:CAA40799.1; PID:g56647
C:Keywords: G protein-coupled receptor; transmembrane protein

```

Query Match	6.1%	Score 268;	DB 2;	Length 1199;
Best Local Similarity	18.8%	Pred. No. 3.1e-12;		
Matches 168;	Conservative 146;	Mismatches 354;	Indels 228;	Gaps
Qy	20	LIASPHLOGGVAGRPDELHIGGIPI-----	-----	AKGGWGGQACMPATRLALD 66
Db	28	LLAGASSORSVARMDGVIIIGALFSVHHQPPAEKVPKCKGRETREQYGIORVEAMFHTLD 87		
Qy	67	DVNPQPNLLPFKLLIHSNDG--ECEPGLGASVMY-----	-----	NLL-----102
Db	88	KINADPVLLPNITLGESEIRDCSWHSSVALEQSIIEFRDLSIRDEKDLNRLCPDGOTL 147		
Qy	103	-----YNPQKMLMLLAGCGTCTTVAEAKMWNILVICYGASSPALSCKRPPTLFRTHPS 158		
Db	148	PPGRTRKPIAGVIGPSSSVAIQVNLQLQLFPQIAYSATSIDLSDTKTYKTYFLRVPS 207		
Qy	159	ATVHNPTFIKLMKKEGWSRVAILLQAAEEVFISTVEDLENRCMEAGVEIVTRQSFSLSDPT 218		
Db	208	DTLQARAMDILVKRYNTWTVSAVHTEGNYGSGMDAPKEAAOEGLCIAHSDKIYSNAGE 267		
Qy	219	-----AVNLRRO--DARIIVGLFVYVAARVLCEWTKQOYLGRAHVWFFIYGWEDN--- 268		
Db	268	KSFDELLAKLERLPKARVVVCFEGMTVRGLLSAMRRILGWVGEFSLIGSDGADRDEVI 327		
Qy	269	-WYEVNLIKAEGITCTVEQMRIA-----	-----	EGHLTTEAL-----WMNONNOTTISGMTAE 315
Db	328	EGYEVEANG-GITIKLOSPEVRSFDDYFLKURLDTNTRNPWFPEFWOHRQCPRLPGHLE 386		





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:13:08 ; Search time 14.82 Seconds  
(without alignments)  
2078.168 Million cell updates/sec

Title: US-09-715-962-2  
Perfect score: 4374  
Sequence: 1 MRKDMTSDGAVTFWIFLLCL.....LINSSAHATPAATLAITQGE 840

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2031.5	46.4	960	1	GBR1_MOUSE
2	2030.5	46.4	961	1	GBR1_HUMAN
3	2004	45.8	991	1	GBR1_RAT
4	1290	29.5	941	1	GBR2_HUMAN
5	1286	29.4	940	1	GBR2_RAT
6	366.5	8.4	976	1	MGR_DROME
7	361	8.3	908	1	MGR8_RAT
8	360	8.2	908	1	MGR8_HUMAN
9	356.5	8.2	912	1	MGR4_RAT
10	355	8.1	908	1	MGR8_MOUSE
11	355	8.1	915	1	MGR7_HUMAN
12	353	8.1	912	1	MGR4_HUMAN
13	353	8.1	915	1	MGR7_RAT
14	334.5	7.6	871	1	MGR6_RAT
15	333	7.6	879	1	MGR3_RAT
16	323	7.4	877	1	MGR3_HUMAN
17	322	7.4	872	1	MGR2_HUMAN
18	318	7.3	872	1	MGR2_RAT
19	313.5	7.2	877	1	MGR6_HUMAN
20	305	7.0	1203	1	MGR5_RAT
21	297.5	6.8	1212	1	MGR5_HUMAN
22	294	6.7	999	1	MGR1_CAEL
23	276	6.3	1194	1	MGR1_HUMAN
24	268	6.1	1199	1	MGR1_RAT
25	227.5	5.2	1079	1	CASR_MOUSE
26	219.5	5.0	1078	1	CASR_HUMAN
27	212.5	4.9	1079	1	CASR_RAT
28	198.5	4.5	1085	1	CASR_BOVIN
29	184.5	4.2	1047	1	ANPB_RAT
30	181.5	4.1	1047	1	ANPB_BOVIN
31	177.5	4.1	1047	1	ANPB_HUMAN
32	172	3.9	1050	1	ANPB_ANGJA
33	159	3.6	540	1	ANPC_HUMAN

34	156	3.6	1061	1	ANPA_HUMAN	PI0666	homo sapien
35	154	3.5	535	1	ANPC_RAT	P41740	rattus norv
36	147.5	3.4	1057	1	ANPA_RAT	PI8910	rattus norv
37	146	3.3	1057	1	ANPA_MOUSE	PI8293	mus musculus
38	145	3.3	1137	1	CYGL_CAEL	Q09435	caenorhabdi
39	144.5	3.3	536	1	ANPC_MOUSE	P70180	mus musculus
40	142	3.2	537	1	ANPC_BOVIN	PI0730	bos taurus
41	137.5	3.1	836	1	GLK1_MOUSE	Q60934	mus musculus
42	137.5	3.1	1103	1	CYGF_BOVIN	O02740	bos taurus
43	132.5	3.0	1108	1	CYGF_HUMAN	P51841	homo sapien
44	128	2.9	918	1	GLK1_HUMAN	P39086	homo sapien
45	128	2.9	1110	1	CYGX_RAT	P51839	rattus norv

#### ALIGNMENTS

RESULT	1
GBR1_MOUSE	
ID	GBR1_MOUSE STANDARD; PRT; 960 AA.
AC	Q9WV18; Q9WV15; Q9WV16; Q9WV17; Q9WU48;
DT	20-AUG-2001 (Rel. 40, Created)
DT	20-AUG-2001 (Rel. 40, Last sequence update)
DT	20-AUG-2001 (Rel. 40, Last annotation update)
DE	GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 1 PRECURSOR (GABA-B
DE	RECEPTOR 1) (GABA-B-R1) (GB1).
GN	GABBR1.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A. (ISOFORM 1A).
RP	MEDLINE=20237752; PubMed=10773016;
RA	Sullivan R., Chateaufneuf A., Coulombe N., Kolakowski L.F. Jr.,
RA	Johnson M.P., Hebert T.E., Ethier N., Belley M., Metters K.,
RA	Abramovitz M., O'Neill G.P., Ng G.Y.K.;
RT	"Coexpression of full-length gamma-aminobutyric acid(B) (GABA(B))
RT	receptors with truncated receptors and metabotropic glutamate
RT	receptor 4 supports the GABA(B) heterodimer as the functional
RT	receptor.";
RT	J. Pharmacol. Exp. Ther. 293:460-467(2000).
RN	[2]
RP	SEQUENCE FROM N.A. (ISOFORMS 1B; 1C AND 1D).
RA	Younger R.;
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A. (ISOFORM 1B).
RA	Lamp K., Humeny A., Nikolic Z., Becker C.-M.;
RT	"Cloning of the murine GABABR1b receptor.";
RL	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN	[4]
RP	SEQUENCE FROM N.A. (ISOFORM 1A).
RA	Humeny A., Lamp K., Nikolic Z., Becker C.-M.;
RT	"Mouse GABA-B receptor cDNA sequence.";
RL	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN	[5]
RP	RIA-R2 INTERACTION.
RX	MEDLINE=99102694; PubMed=9872744;
RA	Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,
RA	Kornau H.-C.;
RT	"Role of heteromer formation in GABAB receptor function.";
RL	Science 283:74-77(1999).
CC	-!- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
CC	MEDIATED BY G-PROTEINS THAT INHIBITS ADENYL CYCLASE ACTIVITY,
CC	STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
CC	INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES
CC	INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
CC	FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
CC	GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
CC	HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
CC	GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
CC	INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE



QY 499 IOSHPVNTIMLGVIIICLLSVILLGDGRFVSPPEYKPCIOARAWLLSTGFTLAYGAM 558  
 Db 621 IONSOPNLNNITAVGCSLALAAFPVLDGVIHIGRSQFPFYCOARLWLLGLFSLGYGSM 680  
 QY 559 FSKVVRVHREFTK--AKTDPKPKVPWKLVTMVSGLLSIDVLVLLSWQIFDPLQRYLETF 616  
 Db 681 FTKIWWHTVFTKKEEKWKRLTPWKLYATVGLLVGMDIITLAIWQIVDPLHRTIETF 740  
 QY 617 PLEDVSTDDIKIRPELEHGESQSRNSMWGLVYGFGLVLVFLAYETRSIKYKQIN 676  
 Db 741 AKERPEDI-DVSIPLQLEHSCSKMNTWLGIFYGKGLLLGLIFLAYETKSVSTEKIN 799  
 QY 677 DSRVYGSIIYVWVLCITAPVGVWIASQDASFALAVIFCPCLSMLLIFVPKVIEW 736  
 Db 800 DHRAVGMAIYNVAVLCITAPVTMTLSSQDAAFAFASLAIYFSSYITLVLFVPMRRL 859  
 QY 737 IRHP--KDKAESKYNPDSAISKDEERYOKLVTEQELQRLITQKEEIRVLRQRLVER 793  
 Db 860 ITRGEWQSEADTKTGSTNNNEEKSRLLKEKRELEKIIEKERVSELRHQIQR 918  
 RESULT 2  
 GBRL\_HUMAN  
 ID GBRL\_HUMAN STANDARD; PRT; 961 AA.  
 AC Q9UBS5; O95375; O9UQ00; O96022; O95975; O95468;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE GAMMA-AMINO-BUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 1 PRECURSOR (GABA-B  
 RECEPTOR 1) (GABA-B-R1) (GB1).  
 GN GABBR1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).  
 RC TISSUE=Cerebellum;  
 RX MEDLINE=99061981; PubMed=9844003;  
 RA Kaupmann K., Schuler V., Mosbacher J., Bischoff S., Bittiger H.,  
 Held J., Froestl W., Leonhard S., Pfaff T., Karschin A., Bettler B.;  
 RT "Human gamma-aminobutyric acid type B receptors are differentially  
 expressed and regulate inwardly rectifying K+ channels.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:14991-14996(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1A; 1B AND 1C).  
 RC TISSUE=Cerebellum;  
 RX MEDLINE=99087321; PubMed=9872316;  
 RA White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H.,  
 Barnes A.A., Emson P., Foord S.M., Marshall F.H.;  
 RT "Heterodimerization is required for the formation of a functional  
 GABA(B) receptor.";  
 RL Nature 396:679-682(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1A).  
 RC TISSUE=Brain;  
 RA Stroop U., Raming K.;  
 RT "Human mRNA for GABA-B1a receptor.";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1A).  
 RC TISSUE=Fetal brain;  
 RX MEDLINE=98440782; PubMed=9753614;  
 RA Grifa A., Totaro A., Rommens J.M., Carella M., Roetto A., Borgato L.,  
 Zelante L., Gasparini P.;  
 RT "GABA (gamma-amino-butyric acid) neurotransmission: identification and  
 fine mapping of the human GABAB receptor gene.";  
 RL Biochem. Biophys. Res. Commun. 250:240-245(1998).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 1A).  
 RX MEDLINE=99014802; PubMed=9798068;  
 RA Goei V.L., Choi J., Ahn J., Bowlus C.L., Raha-Chowdhury R.,

RA Gruen J.R.;  
 RT "Human gamma-aminobutyric acid B receptor gene: complementary DNA  
 cloning, expression, chromosomal location, and genomic organization.";  
 RL Biol. Psychiatry 44:659-666(1998).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 1C).  
 RC TISSUE=Cerebellum;  
 RA Fraser N.J.;  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B), AND VARIANTS V-20 AND S-489.  
 RC TISSUE=Fetal brain;  
 RX MEDLINE=20184230; PubMed=9933300;  
 RA Peters H.C., Kemmer G., Voiz A., Kaupmann K., Ziegler A., Bettler B.,  
 Epplen J.T., Kamber T., Riess O.;  
 RT "Mapping, genomic structure, and polymorphisms of the human GABAB1  
 receptor gene: evaluation of its involvement in idiopathic  
 generalized epilepsy.";  
 RL Neurogenetics 2:47-54(1998).  
 RN [8]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).  
 RA Younger R.;  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [9]  
 RP SEQUENCE FROM N.A. (ISOFORM 1A).  
 RC TISSUE=Cerebellum;  
 RX MEDLINE=99108069; PubMed=9889352;  
 RA Makoff A.;  
 RT "Molecular cloning of human GABAB1 and its tissue distribution.";  
 RL Brain Res. Mol. Brain Res. 64:137-140(1999).  
 RN [10]  
 RP SEQUENCE FROM N.A. (ISOFORM 1E).  
 RC TISSUE=Prostate;  
 RX MEDLINE=20493604; PubMed=10906333;  
 RA Schwarz D.A., Barry G., Eliasof S.D., Petroski R.E., Conlon P.J.,  
 Maki R.A.;  
 RT "Characterization of gamma-aminobutyric acid receptor GABAB(1e), a  
 GABAB(1) splice variant encoding a truncated receptor.";  
 RL J. Biol. Chem. 275:32174-32181(2000).  
 RN [11]  
 RP VARIANTS VAL-20 AND SER-489.  
 RX MEDLINE=99332163; PubMed=10402495;  
 RA Sander T., Peters C., Kaemmer G., Samochowiec J., Zirra M.,  
 Mischke D., Ziegler A., Kaupmann K., Bettler B., Epplen J.T.,  
 Riess O.;  
 RT "Association analysis of exonic variants of the gene encoding the  
 GABAB receptor and idiopathic generalized epilepsy.";  
 RL Am. J. Med. Genet. 88:305-310(1999).  
 RN [12]  
 RP R1A-R2 INTERACTION.  
 RX MEDLINE=20237752; PubMed=10773016;  
 RA Sullivan R., Chateaufort A., Coulombe N., Kolakowski L.F. Jr.,  
 Johnson M.P., Hebert T.E., Ethier N., Belley M., Metters K.,  
 Abramovitz M., O'Neill G.P., Ng G.Y.K.;  
 RT "Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B))  
 receptors with truncated receptors and metabotropic glutamate  
 receptor 4 supports the GABA(B) heterodimer as the functional  
 receptor.";  
 RL J. Pharmacol. Exp. Ther. 293:460-467(2000).  
 RN [13]  
 RP R1A-R2 INTERACTION.  
 RX MEDLINE=99102694; PubMed=9872744;  
 RA Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,  
 Kornau H.-C.;  
 RT "Role of heteromer formation in GABAB receptor function.";  
 RL Science 283:74-77(1999).  
 CC -1- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS  
 MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,  
 CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,  
 CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES  
 CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE  
 CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC  
 CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING

CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC  
 CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT  
 CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE  
 CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN  
 CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM  
 CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND  
 CC ANTINOCICEPTION. ACTIVATED BY (-)-BACLOFEN, CGP27492 AND BLOCKED  
 CC BY PHACLOFEN.  
 CC  
 CC -!- FUNCTION: ISOFORM 1E FUNCTION MAY BE TO REGULATE THE AVAILABILITY  
 CC OF FUNCTIONAL GABA-B-RIA/GABA-B-R2 HETERODIMERS BY COMPETING FOR  
 CC GABA-B-R2 DIMERIZATION. THIS COULD EXPLAIN THE OBSERVATION THAT  
 CC CERTAIN SMALL MOLECULE LIGANDS EXHIBIT DIFFERENTIAL AFFINITY FOR  
 CC CENTRAL VERSUS PERIPHERAL SITES.  
 CC  
 CC -!- COFACTOR: REQUIRES CALCIUM FOR HIGH AFFINITY BINDING TO GABA.  
 CC  
 CC -!- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH  
 CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO  
 CC HAPPEN. ISOFORM 1E (WITHOUT C-TERMINAL INTRACELLULAR DOMAIN) IS  
 CC UNABLE TO DIMERIZE VIA A COILED-COIL INTERACTION WITH GABA-B-R2.  
 CC  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER  
 CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A  
 CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE  
 CC PLASMA MEMBRANE. ISOFORM 1E CAN ALSO BE SECRETED.  
 CC  
 CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; 1A (SHOWN HERE), 1B, 1C, 1D AND  
 CC 1E/TRUNCATED; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORMS  
 CC CORRESPONDING TO THE FULL RECEPTOR ARE ESSENTIALLY FOUND IN THE  
 CC CENTRAL NERVOUS SYSTEM (CNS). ISOFORM 1E IS THE MAJOR ISOFORM IN  
 CC ALMOST ALL PERIPHERAL TISSUES. IT MAY ACT AS AN ANTAGONIST OF  
 CC GABA-B RECEPTORS, BEING ABLE TO DISRUPT THE NORMAL ASSOCIATION  
 CC BETWEEN ISOFORM 1A AND GABA-B-R2.  
 CC  
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN AND WEAKLY IN HEART,  
 CC SMALL INTESTINE AND UTERUS. MOSTLY EXPRESSED IN GRANULAR CELL AND  
 CC MOLECULAR LAYER FOR ISOFORM 1A AND IN PURKINJE CELLS FORM ISOFORM  
 CC 1B. ISOFORM 1E IS PREDOMINANTLY EXPRESSED IN PERIPHERAL TISSUES AS  
 CC KIDNEY, LUNG, TRACHEA, COLON, SMALL INTESTINE, STOMACH, BONE  
 CC MARROW, THYMUS AND MAMMARY GLAND.  
 CC  
 CC -!- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION  
 CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 2. THE  
 CC LINKER REGION BETWEEN THE TRANSMEMBRANE DOMAIN 3 (TM 3) AND THE  
 CC TRANSMEMBRANE DOMAIN 4 (TM 4) PROBABLY PLAY A ROLE IN THE  
 CC SPECIFICITY FOR G-PROTEIN COUPLING.  
 CC  
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
 CC GABA-B RECEPTOR SUBFAMILY.  
 CC  
 CC -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC -----  
 CC DR EMBL; AJ225028; CAA12359.1; -  
 CC DR EMBL; AJ225029; CAA12360.1; -  
 CC DR EMBL; AJ212185; CAA09939.1; -  
 CC DR EMBL; AJ012186; CAA09940.1; -  
 CC DR EMBL; AF099148; AAC98508.1; -  
 CC DR EMBL; Y11044; -; NOT ANNOTATED\_CDS.  
 CC DR EMBL; AJ012187; CAA09941.1; -  
 CC DR EMBL; AJ010170; CAA09031.1; -  
 CC DR EMBL; AJ010171; CAA09031.1; JOINED.  
 CC DR EMBL; AJ010172; CAA09031.1; JOINED.  
 CC DR EMBL; AJ010173; CAA09031.1; JOINED.  
 CC DR EMBL; AJ010174; CAA09031.1; JOINED.  
 CC DR EMBL; AJ010175; CAA09031.1; JOINED.  
 CC DR EMBL; AJ010176; CAA09031.1; JOINED.  
 CC DR EMBL; AJ010177; CAA09031.1; JOINED.  
 CC DR EMBL; AJ010178; CAA09031.1; JOINED.  
 CC DR EMBL; AJ010179; CAA09031.1; JOINED.  
 CC DR EMBL; AJ010180; CAA09031.1; JOINED.  
 CC DR EMBL; AJ010181; CAA09031.1; JOINED.  
 CC DR EMBL; AJ010182; CAA09031.1; JOINED.  
 CC DR EMBL; AJ010183; CAA09031.1; JOINED.

DR EMBL; AJ010184; CAA09031.1; JOINED.  
 DR EMBL; AJ010185; CAA09031.1; JOINED.  
 DR EMBL; AJ010186; CAA09031.1; JOINED.  
 DR EMBL; AJ010187; CAA09031.1; JOINED.  
 DR EMBL; AJ010188; CAA09031.1; JOINED.  
 Query Match 46.4%; Score 2030.5; DB 1; Length 961;  
 Best Local Similarity 49.3%; Pred. No. 8.9e-148;  
 Matches 384; Conservative 152; Mismatches 220; Indels 23; Gaps 8;  
 QY 24 PHLQGGVAGRPDE--LHIGGFFIAGKGGWGGQACMPATRLALDDYNNKPNLLPGFKLI 81  
 Db 155 PHQVNRTPHSERRAVYIGALFPM--GHPGGQACQAPVEMALEVDYNSRDILPDYELK 212  
 QY 82 LHSNDSCEPEGLGASVMNLYNKPQLMLLAGCSTVCTTVAEAAKMNWNLIVLCYGASSP 141  
 Db 213 LIHDSKCDPGQATKYLLEYLNDPIKIILMPGSCSSVTLVAEAAKMNWNLIVLSYGSSP 272  
 QY 142 ALSDRKRPFTLFRTHPSATVHNPTRIKLMKFGHSRVAILQQAEEVFISIVEDLENCRME 201  
 Db 273 ALSNRQRPFTFFTHPSATLHNPTRVKLFKMGWKKIATIQQTTEVFVFTLDDLEVRKE 332  
 QY 202 AGVEIVTRQSFSLDPTDAVRLNRQDARIIVGLFVVAARVLCMTCYKQOOLYGRAHWFF 261  
 Db 333 AGIEIFRQFFSDPVPVNLKQDARIIVGLFYEARKVCEVYKERLFGKYYWFL 392  
 QY 262 IGWYEDNMYEVNLKAEGITCTVEQMRTAAEGHLTTEALMNNQNTTISGMTAEFEHRRL 321  
 Db 393 IGWYADNWFKI--YDPSINCTVDDEMTAEVGHITTEIVMLNPANTRTSNNTSQEFVEKL 450  
 QY 322 NQALIEGYDINHDPDE---GYQEAFLAYDAVMSVALAFNKTMRITTTGKSLRDTYTT 378  
 Db 451 TKRL-----KRHPETGGFOEPLAYDAIWAALALANKTSGGSGRGRLEDENYN 501  
 QY 379 DKEIADIEYAMNSTQFLGYSGVVAFFSQGDRIALTOEQMIDKYEKLGYDQLDNL 438  
 Db 502 NQITDQIYRAMNSSSEFVSGHVVFDASGRMAWTLIEQLQGGSYKKIGYDSTKDDL 561  
 QY 439 WLNTQEWIGGKVPQDRTIVTHLVTSVLPFCVMCTISSCGIFVAFALIIFNWKNHRRV 498  
 Db 562 WSKTDKWWGGPPADQTLVTKTRFLSQKLFISSVLSLGLVLAIVCLSFNIYNSHVRV 621  
 QY 499 IQSSHPVCNTIMLGVVLIISVILLGLDGRFVSPPEEPKICQARAWLLSTGFLAYGAM 558  
 Db 622 IQNSQPNLNLITAVGCSLALAAVPLGLDGYHIGRNQFPFVFCQARLMLLGLGFLSGVGM 681  
 QY 559 FSKVMVRHRTTK--AKTDPKKKVPEPKLYTMVSGLLSIDLVLLSWQIFDPLQRYLET 616  
 Db 682 FTKIWWVHTVFTKKEEKWKRTLEPKLYATVGLLVGMDVLTALWQIVDPLHRTIETF 741  
 QY 617 PLEDVSTTDDIKIRPELEHCSQRNSMWGLVYGFKGLILVFLGLAYETRSIKVQIN 676  
 Db 742 AKEPKEDI-DVSLPQLEHCSSRKMTWLGIYGYKGLLLGLLGLFLAYETKSVSTEKIN 800  
 QY 677 DSRVGMSTYNNVVVLCITAPVGMVIAQQDASAFVALAVIFCCFLSMLLIFFPKVIEV 736  
 Db 801 DHRVAGMALYNVAVLCITAPVTMLSSQDQAAFAFASLAVFSSYITLVVLFVPMRRL 860  
 QY 737 IRHP--KDKAESKYNPDISAISKEDEERYQKLVTEQOLRLITOKEEKIRVQLRQLVER 793  
 Db 861 ITRGEWQSEAQDTMKTGSSSTNNNEEKSRLLLEKENRELEKTIABKEKRVSELRLHQLSR 919  
 RESULT 3  
 GBRL\_RAT  
 ID GBRL\_RAT STANDARD; PRT; 991 AA.  
 AC Q9Z004; O08620; O08621; Q9Z0F9; Q9Z308;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 1 PRECURSOR (GABA-B  
 DE RECEPTOR 1) (GABA-B-R1) (GB1).  
 GN GABBR1.

OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).  
 RC STRAIN-RICO; TISSUE=Brain cortex, and Cerebellum;  
 RX MEDLINE=9722131; PubMed=9069281;  
 RA Kaupmann K., Huggel K., Heid J., Flor P.J., Bischoff S., Mickel S.J.,  
 RA McMaster G., Angst C., Bittiger H., Froestl W., Bettler B.;  
 RT "Expression cloning of GABA(B) receptors uncovers similarity to  
 RT metabotropic glutamate receptors.";  
 RL Nature 386:239-246(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1C AND 1D).  
 RC TISSUE=Cerebellum;  
 RX MEDLINE=99092370; PubMed=9875211;  
 RA Isomoto S., Kaibara M., Sakurai-Yamashita Y., Nagayama Y., Uezono Y.,  
 RA Iano K., Taniyama K.;  
 RT "Cloning and tissue distribution of novel splice variants of the rat  
 RT GABAB receptor.";  
 RL Biochem. Biophys. Res. Commun. 253:10-15(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1E).  
 RC STRAIN-Wistar; TISSUE=Hippocampus;  
 RX MEDLINE=99388283; PubMed=10457184;  
 RA Pfaff T., Malitschek B., Kaupmann K., Prezeau L., Pin J.-P.,  
 RA Bettler B., Karschin A.;  
 RT "Alternative splicing generates a novel isoform of the rat  
 RT metabotropic GABA(B)R1 receptor.";  
 RL Eur. J. Neurosci. 11:2874-2882(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1A), AND R1A-R2 INTERACTION.  
 RC TISSUE=Brain;  
 RX MEDLINE=99175124; PubMed=10075644;  
 RA Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan R.,  
 RA Kargman S., Chateaufort A., Tsukamoto N., McDonald T., Whiting P.,  
 RA Mezey E., Johnson M.P., Liu O., Kolakowski L.F. Jr., Evans J.F.,  
 RA Bonner T.I., O'Neill G.P.;  
 RT "Identification of a GABAB receptor subunit, gb2, required for  
 RT functional GABAB receptor activity.";  
 RL J. Biol. Chem. 274:7607-7610(1999).  
 RN [5]  
 RP TISSUE DISTRIBUTION.  
 RX MEDLINE=20121644; PubMed=10658574;  
 RA Belley M., Sullivan R., Reeves A., Evans J.F., O'Neill G.P.,  
 RA Ng G.Y.K.;  
 RT "Synthesis of the nanomolar photoaffinity GABA(B) receptor ligand CGP  
 RT 71872 reveals diversity in the tissue distribution of GABA(B) receptor  
 RT forms.";  
 RL Bioorg. Med. Chem. 7:2697-2704(1999).  
 RN [6]  
 RP R1A-R2 INTERACTION.  
 RX MEDLINE=99102694; PubMed=9872744;  
 RA Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,  
 RA Kornau H.-C.;  
 RT "Role of Heteromer Formation in GABA-B Receptor Function.";  
 RL Science 283:74-77(1999).  
 RN [7]  
 RP MUTAGENESIS OF SER-247; SER-268 AND SER-269.  
 RX MEDLINE=20159055; PubMed=10692480;  
 RA Galvez T., Urwyler S., Prezeau L., Mosbacher J., Joly C.,  
 RA Malitschek B., Heid J., Brabet I., Froestl W., Bettler B.,  
 RA Kaupmann K., Pin J.-P.;  
 RT "Ca(2+) requirement for high-affinity gamma-aminobutyric acid (GABA)  
 RT binding at GABA(B) receptors: involvement of serine 269 of the  
 RT GABA(B)R1 subunit.";  
 RL Mol. Pharmacol. 57:419-426(2000).  
 CC [1] FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS  
 CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYL CYCLASE ACTIVITY,  
 CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,  
 CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES  
 CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE

CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC  
 CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING  
 CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC  
 CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT  
 CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE  
 CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN  
 CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM  
 CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND  
 CC ANTINOCICEPTION.  
 CC [1] COFACTOR: REQUIRES CALCIUM FOR HIGH AFFINITY BINDING TO GABA.  
 CC [1] SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH  
 CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO  
 CC HAPPEN.  
 CC [1] SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER  
 CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A  
 CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE  
 CC PLASMA MEMBRANE.  
 CC [1] ALTERNATIVE PRODUCTS: 5 ISOFORMS; 1A, 1B, 1C, 1D AND 1E (SHOWN  
 CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC [1] TISSUE SPECIFICITY: ISOFORMS 1A, 1B AND 1C ARE EXPRESSED IN  
 CC TESTIS, STOMACH, SPINAL CORD AND BRAIN INCLUDING CEREBRAL CORTICAL  
 CC LAYERS, PYRAMIDAL CELL LAYERS OF THE HIPPOCAMPUS, GRANULAR CELL  
 CC LAYERS OF THE DENTATE GYRUS, BASAL GANGLIA, CEREBELLUM  
 CC (PREDOMINANTLY IN PURKINJE CELLS FOLLOWED BY GRANULAR LAYER).  
 CC ISOFORM 1B IS ALSO EXPRESSED IN KIDNEY AND LIVER. ISOFORM 1D IS  
 CC EXPRESSED IN FOREBRAIN, CEREBELLUM, EYE, KIDNEY, AND URINARY  
 CC BLADDER.  
 CC [1] DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION  
 CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 2. THE  
 CC LINKER REGION BETWEEN THE TRANSMEMBRANE DOMAIN 3 (TM 3) AND THE  
 CC TRANSMEMBRANE DOMAIN 4 (TM 4) PROBABLY PLAY A ROLE IN THE  
 CC SPECIFICITY FOR G-PROTEIN COUPLING.  
 CC [1] SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
 CC GABA-B RECEPTOR SUBFAMILY.  
 CC [1] SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.  
 CC [1] CAUTION: ISOFORM 1E HAS BEEN CALLED 1C IN REF. 3.  
 CC -----  
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 CC -----  
 CC EMBL; Y10369; CAA71398.1; -;  
 CC EMBL; Y10370; CAA71399.1; -;  
 CC EMBL; AB016160; BAA34708.1; -;  
 CC EMBL; AB016161; BAA34709.1; -;  
 CC EMBL; AF110797; AAD19656.1; -;  
 CC EMBL; AF110796; AAD19655.1; JOINED.  
 CC EMBL; AF110797; AAD19657.1; -;  
 CC EMBL; AF110796; AAD19657.1; JOINED.  
 CC EMBL; AF110797; AAD19658.1; -;  
 CC EMBL; AF110796; AAD19658.1; JOINED.  
 CC EMBL; AF110797; AAD19659.1; -;  
 CC EMBL; AF110796; AAD19659.1; JOINED.  
 CC HSSP; P10998; IVVC.  
 CC InterPro; IPR001828; ANF\_receptor.  
 CC InterPro; IPR000337; GPCR\_Mgr.  
 CC InterPro; IPR000436; Sushu\_SCR\_CCP.  
 CC Pfam; PF00003; 7tm\_3; 1.  
 CC Pfam; PF01094; ANF\_receptor; 1.  
 CC Pfam; PF00084; sushu; 2.  
 CC PRINTS; PR01177; GABABRECEPTR.  
 CC PRINTS; PR01176; GABABRECEPTR.  
 CC SMART; SM00032; CCP; 2.  
 CC PROSITE; PS00379; G\_PROTEIN\_RECEP\_F3\_1; FALSE\_NEG.  
 CC PROSITE; PS00380; G\_PROTEIN\_RECEP\_F3\_2; FALSE\_NEG.  
 CC PROSITE; PS00981; G\_PROTEIN\_RECEP\_F3\_3; FALSE\_NEG.  
 CC PROSITE; PS00259; G\_PROTEIN\_RECEP\_F3\_4; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 CC Postsynaptic membrane; Coiled coil; Repeat; Alternative splicing.  
 CC KW









Query Match 29.5%; Score 1290; DB 1; Length 941;  
Best Local Similarity 33.9%; Pred. No. 6.2e-91;  
Matches 286; Conservative 170; Mismatches 332; Indels 56; Gaps 18;

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QY 18 LCLASPHLQGGVAGRP-----DELHIGGIPPI---AGKGGWQGGACMPATRLALDDV 68
DB 31 LLLPLAPGAWGARGAPRPPSPPLSLINGLPLTEVAKGSI--GRGVLPVELAIEQI 88
QY 69 NKQPNLLPGFKLILHNSDECEPGGLGASVYMYNLLYNKPKQLMLLAG-CSTVCTTVAEAAK 127
DB 89 RNESLLRPVF-LDLRLYDECDNAKGLKAFYDAIKYGNHLMVGGVCPSTVTSIIAESLQ 147
QY 128 MWNLVLCYGASSPALSRRKPTFLTRHPSATVHNPTRIKLMKKGWSRVAILQQAEEV 187
DB 148 GWNVLQSFATTPVLAADKKYFYFRTPVPSDNAVNPAILKLLKHYQKWRKLTQDVQR 207
QY 188 FISTVEDLENRCMEAGVEITVQSFSLSDPTDAVRNLRRODARLIIVGLFYVVAARRVLCM 247
DB 208 FSEVRNDLTGVYGEDIELSDTESFSDNPTCSVKLKGNDVRIILGQFQDNMAAKVPCA 267
QY 248 YKQQLYGRAHVWFFIGWYEDNNYE-VNLKAEGITCTVEQMRIAAEGHLTTEALMWNQNNQ 306
DB 268 YEENYGSYQWILPGWEPSEWQVHTTEANSRCLRNLLAAEGYIGVDFEPLSKQI 327
QY 307 TTISGMTAEFRHLRNQALIEGYDINHDPYEGYQEAFLAYDAVMSVALAFNKTWERL- 365
DB 328 KTISGKTPOQYEREYNKRGSGVPSKFH-----GY-----AYDGIWIAKTLQRAMETHL 377
QY 366 -TTGKSLRDFYTDKEIADEIYAAMNSTQFLGVSGVAFSSQGDRIALTQIEQMDGKY 424
DB 378 ASSRQRQDFNYDHTLGRILNANMETNFFGVTVQGVFRN-GERMGTKFTQFQDSRE 436
QY 425 EKLGYDITOLDNLWLN-TEQWIGKGVPODRTIVTHVLRVSLPLFCMCTISSCGIFVA 483
DB 437 KVGGEYNAVADTLEINDTIRFGGSEPPKDKTIIQLRKLISLPLSILSALTILGIMA 496
QY 484 FALIIFNIWKKHRRVYQSSHPVCNTIMLFGVILCLISVILGIDGRFVSPPEEPKICQAR 543
DB 497 SAFLEFNKNRKNOKLIKMSPPYNNLILGGLMSYASIFLFGLDGSGFVSEKTFETLCTVR 556
QY 544 AWLLSTGFTLAYGAFSKWVRVHRFTTKAKTDPKKVPKLYTMVSGLLSIDLVILLWS 603
DB 557 TWILTVGYTAFGAFKTRVHAIFPKVKM-KKKI1KDKQLLVIVGGMLLIDLCILICW 615
QY 604 QIFDPLQRYLETFPLE-DEPVSITDIIKIRPELEHCEFSQNSMWGLVYGKGLILVPLGL 662
DB 616 QAVDPLRRIVEKYMEDPDAGR--DISIRPLEHCENTHTIWLGIYVAYKGLMLPGCF 673
QY 663 LAYETRSIKVKQINDSYGMSIYVYVLCITAPVGMVITASQODASFAFVALAVIPCCF 722
DB 674 LAWETRNVSIPALNDSKYIGMSVYNGVINCIIAGAAVSFLTRDQPNVQFCIVALVIFCST 733
QY 723 LSWLLIFVPKVIETVRHP-----KDKAESKNPD-SAIKSEDEERYQKLV 767
DB 734 ITFLVFPVKLTLRNPDAATQNRFRFQTONQKEDSKTSTSVTSVNOASTSRLEGLOS 793
QY 768 ENQQLRLITQKEEKIRVLRQLVERGDAGT-----ELNGATCVASAAVATTQSPA 819
DB 794 ENHRUMKITEKDLKLEVTMLQDTPPE-KTYYIKONHYQELNDILNLTFTSTGGKA 852
QY 820 SLIN 823
DB 853 ILKN 856
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RESULT 5

GBR2\_RAT STANDARD; PRT; 940 AA.

AC O88871; Q9QWU2; Q9JK36;

DT 20-AUG-2001 (Rel. 40, Created)

DT 20-AUG-2001 (Rel. 40, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 2 PRECURSOR (GABA-B  
DE RECEPTOR 2) (GABA-B-R2) (GB2) (GABABR2).  
GN GABBR2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Hypothalamus;  
RX MEDLINE=99087320; PubMed=9872315;  
RA Jones K.A., Borowsky B., Tamm J.A., Craig D.A., Durkin M.M., Dai M.,  
RA Yao W.-J., Johnson M., Gunwaldsen C.A., Huang L.-Y., Tang C., Shen Q.,  
RA Branchek T.A., Gerald C.;  
RT "GABA(B) receptors function as a heteromeric assembly of the subunits  
RT GABA(B)R1 and GABA(B)R2.";  
RL Nature 396:674-679(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain cortex, and Cerebellum;  
RX MEDLINE=99087322; PubMed=9872317;  
RA Kaupmann K., Malitschek B., Schuler V., Heid J., Froestl W., Beck P.,  
RA Mosbacher J., Bischoff S., Kulik A., Shigemoto R., Karschin A.,  
RA Bettler B.;  
RT "GABA-B receptor subtypes assemble into functional heteromeric  
RT complexes.";  
RL Nature 396:683-687(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain cortex;  
RX MEDLINE=20193514; PubMed=10727622;  
RA Clark J.A., Mezey E., Lam A.S., Bonner T.I.;  
RT "Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";  
RL Brain Res. 860:41-52(2000).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Hypothalamus;  
RA Borowsky B., Laz T., Gerald C.;  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP RIA-R2 INTERACTION, AND VARIANTS TYR-337 AND PRO-19 INS.  
RC TISSUE=Hippocampus;  
RX MEDLINE=99102694; PubMed=9872744;  
RA Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,  
RA Kornau H.-C.;  
RT "Role of Heteromer Formation in GABA-B Receptor Function.";  
RL Science 283:74-77(1999).  
CC -1- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS  
CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,  
CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,  
CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES  
CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE  
CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC  
CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING  
CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC  
CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT  
CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE  
CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN  
CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM  
CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND  
CC ANTINOCICEPTION.  
CC -1- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH  
CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO  
CC HAPPEN.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER  
CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A  
CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE  
CC PLASMA MEMBRANE.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN CORTEX, HIPPOCAMPUS, MEDIAL  
CC HABENULA, THALAMUS AND CEREBELLUM. COEXPRESSION IS SEEN IN  
CC CEREBELLUM.



RP SEQUENCE FROM N.A.  
RC STRAIN=OREGON-R;  
RX MEDLINE=96421661; PubMed=8824309;  
RA Parentier M.L., Pin J.P., Bockaert J., Grau Y.;  
RT "Cloning and functional expression of a Drosophila metabotropic  
RT glutamate receptor expressed in the embryonic CNS.";  
RL J. Neurosci. 16:6687-6694(1996).  
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE CNS OF THE LATE EMBRYO.  
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
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CC  
CC EMBL; X9675; CAA67993.1; -.  
DR GCRDb; GCR\_1123; -.  
DR FlyBase; FBgn0019985; Glu-RA.  
DR InterPro; IPR001828; ANF\_receptor.  
DR InterPro; IPR000337; GPCR\_Mgr.  
DR Pfam; PF00003; 7tm\_3; 1.  
DR Pfam; PF01094; ANF\_receptor; 1.  
DR PRINTS; PR00248; GPCRMR.  
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DR PROSITE; PS00983; G\_PROTEIN\_RECEP\_F3\_5; 1.  
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.  
FT SIGNAL 1 25  
FT CHAIN 26 976 METABOTROPIC GLUTAMATE RECEPTOR.  
FT DOMAIN 26 976 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 627 649 I (POTENTIAL).  
FT DOMAIN 650 663 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 664 684 II (POTENTIAL).  
FT DOMAIN 685 695 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 696 714 III (POTENTIAL).  
FT DOMAIN 715 738 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 739 759 IV (POTENTIAL).  
FT DOMAIN 760 782 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 783 804 V (POTENTIAL).  
FT DOMAIN 805 817 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 818 840 VI (POTENTIAL).  
FT DOMAIN 841 850 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 851 876 VII (POTENTIAL).  
FT DOMAIN 877 976 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 112 112 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 216 216 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 386 386 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 491 491 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 524 524 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT SEQUENCE 976 AA; 108457 MW; 2C17B1F9005AF68 CRC64;

Query Match 8.4%; Score 366.5; DB 1; Length 976;  
Best Local Similarity 19.7%; Pred. No. 5.3e-20;  
Matches 203; Conservative 164; Mismatches 383; Indels 281; Gaps 40;  
QY 3 KDMTSDGAVTFWFLCL-----IASP---HLQGGVA-GRPDELHIGGIPPIAGKGGWQG 53  
DB 2 KQNNNGTILVVMVWSRVDLKSPTHODSVSVSLPGDIIILGLFPVHEKG---E 58  
QY 54 GQACMP-----ATRLALDDYNKOPNLLPGFKLILHSNDS----- 87  
DB 59 GAPCGPKVYNRGVRLEAMLYAIDRVNDPNILPGITIGVHILDTCSDRYALNQSLQV 118

QY 88 -----ECEPGIGASVMYNNLLYNKPKQLMLLAGCCTVCTTVAEAAKMNLLVLC 135  
DB 119 RASUNNLDTSGEYECADGSSPOLRKN-ASSGPVFGVGGSSVSLQVALLRLRPHIPOVS 177  
QY 136 YGASSPALSQRKRPPTLFRTHPSATVHNPTRIKLMKFGWSRVAILQAQAEVFISTVDL 195  
DB 178 PASTAKTSLDKTRFDLFAITVPPTFQSFVALVDILKNFNSVYSTIHSEGSYGEVGEAL 237  
QY 196 ENRMEAGVIEIVTRQSFSLSDPTDAV-----RNLRORDARIIVGLFVYVVAARRVLCMEYK 249  
DB 238 HKEATERNVCIATAEKPVSAAADKVFDSIISKLOKKNARGVWLFTRAEDARRIL----- 292  
QY 250 QQLYGRAHVFFIGWY-EDNMYEYNLKAEGI-----TCTVE-QMRTAAE-----GHLTT 296  
DB 293 -QAAKRALNSOPFFHIASDGGKOOKLLEGLEDIAEGAITVELQSEIIADFRYMMQUTP 351  
QY 297 E-----ALMW-----NONNOTTISGMTAEERHRLNOALI 326  
DB 352 ETNORNPFAYWEDTFCVLTSLSVKPDTSNSANSTDNKGIVKAKTECDSDSYRLSEKV- 410  
QY 327 EEGYDINHRYPEGYQEAFLAY--DAVMSVALAF-----NKTMERLTTGKSLRDF 376  
DB 411 --GYE-----QESKTOFVVDVAVAFAYALHNLHNDRCNTQSDQTTETRHLQSES 458  
QY 377 YDKEIADEIYAA-----MNSTQFLVSG-VVAFSSQGDRIALTQI-- 416  
DB 459 VYRKIKISTDTKSOACPDMAVYDGEFNYNNLLANSFIDLAGSEYKFDQDGLARYDILN 518  
QY 417 -----EQMDGKYEKLYGYDTOLDNLSWLNTEBOWIGGKVPQDRTIVTHVLRVSLPLFCVM 472  
DB 519 YQRENSGGYQYKVGKWFNGLQ-----LNSETVVVNKETEQT-----SACSLPCEVGM 568  
QY 473 -----C-----TISGCG-----IF 481  
DB 569 IKKQGDTCWCWICDSCSEFEVYVDEFTCKDGPGLWPYADKLSCYALDIOYMKWNSL 628  
QY 482 VAFALITFNI-----WNKRRVIOQSHPVNTIMLFGVILCISVILLIGIDGRF 530  
DB 629 IPMAIAIFGIALTSIVIVLFAKNHDTPLVRASGRELSYTLFLGLVLCYCNFTAL----- 682  
QY 531 VSPEYPKI--COARAWLLSTGFTLAYGAMFSKVRVHR-FTTKAKTDPK-KKVEPWKLY 586  
DB 683 ---IAKPTIGSCVLORFQGVGFGLIYIYALLTKNRISRIFHSASKSAQRUKYISPOSQV 739  
QY 587 TWSGLLSIDLIVLLSWQIFDPLQRYLETFPLEDPVSTDDIKIRPELECHESQRNSMWL 646  
DB 740 VITTSLIAQVILITMVMVVEP-----PGTFEYPPDRREVILCKIQDMSFLF 787  
QY 647 GLVYGFGLILVFLGLFLAYETRSIKVKOINDSRVGMISYVNVVLCITAPVGVWIASQQ 706  
DB 788 SOLYNN--ILITICTIYAIKTRKIP-ENFNESKFIQFTMTYTCITLWAFAPYFTGNSY 844  
QY 707 DASFAVALAVIFCCFLSMILLIFVPKVIETVRHPKDAESKYNPDALSKEDEERYOKLV 766  
DB 845 EVQTTTLCISLSASVALVCLISPKVILVIFHP-DKNVRKLTWNSTVYRASAANAOGA 903  
QY 767 TENEQALRLITQKEKIRVLRQLRVERGDAGKTE-LNG---ATGVASAATAVTSOP----- 818  
DB 904 PTSSGYSRT-----HAPGTSALTGGAVGTNASSSTLTQNSPHLDE 944  
QY 819 ASLINSNAHAT 829  
DB 945 ASAQTNVAHKT 955  
RESULT 7  
ID MGR8\_RAT STANDARD; PRN; 908 AA.  
AC P70579;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.





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QY 468 -----LFVCMCTI-----SSC----- 478
Db 524 ERKTKVGPCCWHCERCEGYNQVDELSCELCPLDQRPNNMRTGCQIPIIKLEHWSWP 583
QY 479 --GIEFA-----FALLIFNTWKKHRRVIOSSHPCVNTIMLFGVVICLLSVILLGID 527
Db 584 AVVPFVAILGIIATTFVIVTFVRYN-DTPIVRASGRELSVYLLTGIFLCYSITFLM--- 639
QY 528 GRFVSPEYPRKICARALLSTGTFLAYGAMFSKVMRVRHFTTKAK---TDPKKKVEPWK 584
Db 640 --IAAPDTI--ICSFRRVFLGLCMGCFSAALLTKNRHHRFEQKKSWTAP-KFISPAS 594
QY 585 LYTMVSGLLSIDLVLLSQWIFDPLQRYLTFPLEDPVSTTDDIKIRPELEHCEQSQRNSM 644
Db 695 QLVITESLISVOLLGVFWFVVDPPHIIID---YGEQRTLDPEKARGVLK-CDISDLSL 749
QY 645 WLGLVYGFGLIIVFGLFAYETRSIKVQINDSRVGMYSYNNVVLCLITAPVGMVIAS 704
Db 750 ICSL--GYSILLMTCTVYAIKTRGVP-ETFNEAKPIGTMYTTCIILWLAIFIPFGTAQ 806
QY 705 QODASE---AFVALAVIFCCFLSMLLIFFVPKVIEWIRHPKDKAESKYNPDSAISKEDEER 761
Db 807 SAEKMYIQTTLTVSMLSUSASVSGMLYMPKVYIIIFHPQONVQRR-----KRS 855
QY 762 YQKLVTENEQQLRLITKEERIRVLQRQLVERGDAGTGLNGATGVASAAVATTSPASL 821
Db 856 FKAVVTAATMOSKLIQKGNDR-----PNGEVK-SEL-----CESLETWTSKTTY 900
QY 822 INSSAHA 828
Db 901 ISYSNHS 907

RESULT 9
MGR4_RAT STANDARD; PRT; 912 AA.
AC P31423;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 4 PRECURSOR.
GN GRM4 OR GPRC1D OR MGLQR4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92110002; PubMed=1309649;
RA Tanabe Y., Masu M., Ishii T., Shigemoto R., Nakanishi S.;
RT "A family of metabotropic glutamate receptors.";
RL Neuron 8:169-179(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93332699; PubMed=8338667;
RA O'Hara P.J., Sheppard P.O., Thøgersen H., Venezia D., Haldeman B.A.,
RA McGrane V., Houamed K.M., Thomsen C., Gilbert T.L., Mulvihill E.R.;
RT "The ligand-binding domain in metabotropic glutamate receptors is
RT related to bacterial periplasmic binding proteins.";
RL Neuron 11:41-52(1993).
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS. PREDOMINANT
CC EXPRESSION IS SEEN IN THE GRANULE CELLS OF THE CEREBELLUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR6.
CC -----
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CC -----
CC EMBL; M92077; -; NOT_ANNOTATED_CDS.
DR EMBL; M90518; AAA93190.1; -.
DR PIR; JH0563; JH0563.
DR GCRDb; GCR_0352; -.
DR GCRDb; GCR_0363; -.
DR InterPro; IPR001828; ANF_receptor.
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DR PRINTS; PR00248; GPCRGR.
DR PRINTS; PR00593; MTABOTROPICR.
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Db 295 EAARANQTHG---FFWMG--SDSMGSKGAPVLRLEVEAGAVTILPKRMSVRGFDRIYS 349
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RESULT 10
MGR8_MOUSE STANDARD; PRT; 908 AA.
AC P47743;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.
GN GRM8 OR GPRC1H OR MGLUR8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Retina;
RX MEDLINE=95239344; PubMed=7722646;
RA Duvoisin R.M., Zhang C., Ramonell K.;
RT "A novel metabotropic glutamate receptor expressed in the retina and
RT olfactory bulb.";
RL J. Neurosci. 15:3075-3083(1995).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN OLFACTORY BULB,
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CC ACCESSORY OLFACTORY BULB, AND MAMMARY BODY. WEAKER EXPRESSION
CC IN THE RETINA, AND IN SCATTERED CELLS IN THE CORTEX AND HINDBRAIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U17252; AAA68149.1; -.
DR GDB; GCR_1712; -.
DR MGI; MGI:1351345; Gprclh.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCRMR.
DR PRINTS; PR00593; MTABOTROPICR.
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DR PROSITE; PS02059; G_PROTEIN_RECP_F3_4; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Olfaction.
FT SIGNAL 1 33
FT CHAIN 34 908
FT DOMAIN 34 583
FT TRANSMEM 584 608
FT DOMAIN 609 620
FT TRANSMEM 621 641
FT DOMAIN 642 647
FT TRANSMEM 648 668
FT DOMAIN 669 695
FT TRANSMEM 696 716
FT DOMAIN 717 746
FT TRANSMEM 747 768
FT DOMAIN 769 781
FT TRANSMEM 782 803
FT DOMAIN 804 818
FT TRANSMEM 819 843
FT DOMAIN 844 908
FT CARBOHYD 95 95
FT CARBOHYD 298 298
FT CARBOHYD 452 452
FT CARBOHYD 480 480
FT CARBOHYD 565 565
FT SEQUENCE 908 AA; 101413 MW; 4CDD9D35827ED41F CRC64;
POTENTIAL.
METABOTROPIC GLUTAMATE RECEPTOR 8.
EXTRACELLULAR (POTENTIAL).
I (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
II (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
III (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
IV (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
V (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
VI (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
VII (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 908 AA; 101413 MW; 4CDD9D35827ED41F CRC64;
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Query Match 8.1%; Score 355; DB 1; Length 908;
Best Local Similarity 21.0%; Pred. No. 3.6e-19;
Matches 200; Conservative 159; Mismatches 390; Indels 204; Gaps 44;
Qy 13 FWFILCLLIASPHLOGGVAG-RPD-ELHTGGILFFIAGKGGWGOAC-----MP 59
Db 22 YWI--LTMQTHSQEYAHSRDLGDIIIGLFFPVHAKG--ERGVPCGDLKKEGIHRL 77
Qy 60 ATRLALDDVNKQNPILLPGFKL---IL-----HSNDSCEPGL 93
Db 78 AMLYADITNKDPLLNSITLGVRLDTCSDRYALEQSLTFVQALIEKDAVDKNCAGD 137
Qy 94 GASVYNLLYNKPKQL--MLJAGCSTVCTTVAEAAAMNMLIVLCYGASSPALSDRRPFT 151
Db 138 PP-----IFTKPKDISGVIGAASVSIMVANILRFLKIPQISYASTAPELSDNTRYDF 191
Qy 152 LFRTHPSATVNPTRIKLMKKEGWSRVAILQAAEEVFISTVEDLENRCHE-AGVEIVTQ 210
Db 192 FSRVVPDYSQAQAMVDIVTALGNVYSTLASEGNYGESGVFAFTQISREIGGVCAIQSQ 251
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Db 24 LLLCAAARAAAGQEMAPHYSIRIEGDVT-----LGLFPVHAKG--PSGVPQCGDIKREN 74  
QY 58 ----MPATRLALDDVKNQKNLLPGFKL---IL-----HSNDS 87  
Db 75 GTHRLFAMLYALDQINDSDNPLNVTLGARILDTCSRDYALBQSLFTVQALIQKDTSDV 134  
QY 88 ECEPGLGASVMYNLLYNKPKQLMLLAGC--STVCTTVAAEAKMNLVILCYGASSPALS 145  
Db 135 RCTNGEPP-----VFVKPEKVGIVGASGSSVSIWVANILRLFPQIPQISTAPAPELS 188  
QY 146 KRFRPTLTHPSATVHNPTRIKLKKFGSRVAILLQAAEEVISTVEDLRCMEAGVE 205  
Db 189 DRRYDFESRVPPDSFQAQAVDIVRALGWN-----YVSLAS-EGSYGKGV 236  
QY 206 IVTROSFLSDPTDANVNL-----RQDA-----RIIVGLFVVAARRVLC-----EMYKQOL 252  
Db 237 SFTQISKEAGGLCIAGSVIRPQBRKDTIDFDRIIKQLLDTNPSRAVVFANDEDIKQIL 296  
QY 253 YG--RA-HWFFFIQWYEDNW-----YEVNLAEGITCTVEQMRTAAG--HLTTEAL 299  
Db 297 AAKRADQVGHFLWGSWSKINPLHQHEDIAEG-AITIQPKRAVTEGFDAFTSRTL 355  
QY 300 -----MW-----NONQFTTISGMTAEF--RHRLNQALIEGYDINHDPYEGYQEP 345  
Db 356 ENNRNVWFAEYWEENFNCKLTISGKKEDTDRKCTGOERI--GKDSNYEQ--EG--KVQ 409  
QY 346 LAYDAVMSVALAFNKMTMERLTT-----GKSLRDFTYTDKETADEIYAAUNS 392  
Db 410 FVIDAVYAMAHALHMHMKDLCADYRGVCPMEQAGGKKLK-----YIRN 454  
QY 393 TOFLGVSGV-VAFSSOGDRIALTOIQMDIGYKELGYDTQDNLWS-----L 440  
Db 455 VFNESAGTPVMFNKNGD-----APGRYDIFQYQYQNTSNRGYRLIGOWTDELQ 504  
QY 441 NFE--QWIGG--KVP-----L 451  
Db 505 NIEDMQWKGVRIPASVCTLPCKPQQRKTKQGTCCWTCPCDGYQYQFDEMTQCHP 564  
QY 452 -----QDRIVT---HVLRTVSLPLFVCMCTISSCGIFVAFALIIIFNIWNKHR 496  
Db 565 YDQPNENRTGCQDIPILKLEWSPNAV-IPVFLAMLGLIAT-IFVMATFIRYN-----DT 618  
QY 497 RVIOSSHPVCMITMLFGVILCLISVILLGIDGRFVSPPEYPKICQARAWLLSTGFTLAYG 556  
Db 619 PIVRASGRLSVYLLGIFLCYITITFLM-----IAKPD--VAVCSFRFVFLGLGMCISYA 671  
QY 557 AMFSKVMRVHREFTTKAK---TDPKKVPEPKLTYMWSGLLSIDLIVLLSQIDPLQRYL 613  
Db 672 ALLTKNRIYRFEQCKKSVTAP-RLISPTSQLAITSSLSVOLLGVFIWFGVDPNII 730  
QY 614 ETPLEDPVSTDDIKIRPELEHCEQSQRNSMWGLGVYGFKGLILVFLGLFLAYETRSIKVK 673  
Db 731 D-----YDEHKTNPMEQARGVLK-CDITDQLICSL--GYSILLMVTCTVVAIKTRGVP-E 782  
QY 674 QINDSRVCMNSYNNVVCLITAPGVMTVASQODASFAFV-----ALAVIFCFLSMLLI 728  
Db 783 NFNEAKPIGFTYTTICVWLAFTPI--FFCTAQSAREKLYIQTTTLTISMNLSASVALGML 840  
QY 729 FVPKVLIEVRHPKDKAESYNNPDSAISKEDEERYQKLVTENEQILRLITQKEEKIRVLQ 788  
Db 841 YMPKVIILIFHPELNVQKR-----KRSFKAVVTAAATMSSRLSHKPSDR----- 883  
QY 789 RLVERGDAGKTEL 801  
Db 884 ---PNGEAK-TEL 892  
RESULT 12  
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ID MGR4\_HUMAN STANDARD; PRT; 912 AA.  
AC Q14833;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE METABOTROPIC GLUTAMATE RECEPTOR 4 PRECURSOR.  
GN GRM4 OR GPRC1D OR MGLUR4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=96346635; PubMed=8738157;  
RA Makoff A., Lelchuk R., Ozer M., Harrington K., Emsen P.;  
RT "Molecular characterization and localization of human metabotropic  
RL glutamate receptor type 4.";  
RN Brain Res. Mol. Brain Res. 37:239-248(1996).  
[2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98141892; PubMed=9473604;  
RA Wu S., Wright R.A., Rockey P.K., Burgett S.G., Arnold J.S.,  
RA Rostock P.R. Jr., Johnson B.G., Schoepf D.D., Belagaje R.M.;  
RT "Group III human metabotropic glutamate receptors 4, 7 and 8:  
RT molecular cloning, functional expression, and comparison of  
RL pharmacological properties in RGT cells.";  
RN Brain Res. Mol. Brain Res. 53:88-97(1998).  
[3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=95342351; PubMed=7617140;  
RA Flor P.J., Lukic S., Ruegg D., Leonhardt T., Knoepfel T., Kuhn R.;  
RT "Molecular cloning, functional expression and pharmacological  
RT characterization of the human metabotropic glutamate receptor type  
RL 4.";  
RN Neuropharmacology 34:149-155(1995).  
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR  
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE  
CC ACTIVITY.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN THE CEREBELLUM.  
CC EXPRESSED AT LOW LEVELS IN HIPPOCAMPUS, HYPOTHALAMUS AND  
CC THALAMUS. NO EXPRESSION DETECTED IN LIVER.  
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
CC STRONGEST, TO MGLUR6.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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DR EMBL; X80818; CAA56784.1; -;  
DR EMBL; U92457; AAB51762.1; -;  
DR GCRdb; GCR\_1891; -;  
DR GCRdb; GCR\_2069; -;  
DR MIM; 604100; -;  
DR InterPro; IPR001828; ANF\_receptor.  
DR InterPro; IPR000337; GPCR\_Mgr.  
DR Pfam; PF00003; 7tm\_3; 1.  
DR Pfam; PF01094; ANF\_receptor; 1.  
DR PRINTS; PR00248; GPCRMR.  
DR PRINTS; PR00593; MTABOTROPICR.  
DR PRINTS; PR01054; MTABOTROPICR.  
DR PROSITE; PS00979; G\_PROTEIN\_RECEP\_F3\_1; 1.  
DR PROSITE; PS00980; G\_PROTEIN\_RECEP\_F3\_2; 1.  
DR PROSITE; PS00981; G\_PROTEIN\_RECEP\_F3\_3; 1.  
DR PROSITE; PS0259; G\_PROTEIN\_RECEP\_F3\_4; 1.  
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
KW Multigene family.  
FT SIGNAL 1 32 POTENTIAL.  
FT CHAIN 33 912 METABOTROPIC GLUTAMATE RECEPTOR 4.  
FT DOMAIN 33 587 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 588 610 I (POTENTIAL).

FT DOMAIN 611 624 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 625 645 II (POTENTIAL).  
FT DOMAIN 646 656 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 657 675 III (POTENTIAL).  
FT DOMAIN 676 699 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 700 720 IV (POTENTIAL).  
FT DOMAIN 721 750 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 751 772 V (POTENTIAL).  
FT DOMAIN 773 785 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 786 808 VI (POTENTIAL).  
FT DOMAIN 809 821 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 822 847 VII (POTENTIAL).  
FT DOMAIN 848 912 CYTOPLASMIC (POTENTIAL).  
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FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 454 454 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 484 484 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 569 569 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 912 AA; 101867 MW; 4A2F36G3A2EAF5A CRC64;  
Query Match 8.1%; Score 353; DB 1; Length 912;  
Best Local Similarity 18.5%; Pred. No. 5.2e-19;  
Matches 169; Conservative 179; Mismatches 371; Indels 196; Gaps 38;  
QY 13 FWIFL-LCLIAS-----PHLQGGVAGRP-----DELHIGGIFPIAGKGWQGGQAC 57  
Db 10 WVARLPCLLLSLXGPMPSLGRPKGPHMNSIRIDGDIITGLGFPVHGRG--SGKPC 67  
QY 58 -----MPATRLALDVNQPNLLPGFKL-----IL 82  
Db 68 GELKKERGIHRLAMFLFLEIRINDPDLNITLGLARILDTCSRTHALEQSLTFVQALI 127  
QY 83 HSNDECEPGLGASVMYLLNKKPKMLLAGC--STVCTTVAEAKWNVLIVLCYGASS 140  
Db 128 EKDTEVRCGGGPP-----IITKPERVGVGIGASGVSSIMVANILRUFKIPQISYASTA 183  
QY 141 PALSDRRKRFPTLFRTHPSATHNPTRIKMKKFGSRVAIL-----QOAEVEFSTIVE 193  
Db 184 PDLSDNSRYDFSRVSPDTYQOAMVDIVRAKKNVYSTVASESGSYGESGVAEFLQKR 243  
QY 194 DLENRCMEAGVEIVTROSFLSDPTDAVRN--LRQDARIIVGLVYVAARRVLCVMYKQOL 252  
Db 244 EDGVCIAQSVKI--PREPKAGEFKIIRRLLETSNARAVIIFANEDDIRVLEAARRAQ 302  
QY 253 YGRAHVFFIGWYEDNW-----YEVNLKAEG-ITCIVEQMRIAEGHLITTEALMWNQ 304  
Db 303 TGH---FFWMG--SDSWGSKTAPVLHLEEAEGAVTILPKRMSVRGDFRYSRTLDNRR 357  
QY 305 NQTTISGMTAEFRHRLNOALIEGYDI---NHDRYPE--GYOE---APLAYDAVWSVA 355  
Db 358 RNIWFAEFEDNFKLSRHALKSGSHVKKCTNRERICQDSAYEQBGKVQFVIDAVIANG 417  
QY 356 LAFNKTMERLTGKSLRDTFTYDKETIADEIYAAMNSTQFLGVSG--VVAFFSQGD---RI 411  
Db 418 HALHAMRDLCPGRVGL--CFRPMVDGTQLLKLYRNVSFAGIAGNPVTENGADPGRY 475  
QY 412 ALTIQIEMID-GKYEKLG----YDTQLDNLSWLNTEQWIGKV-----PQDR----- 454  
Db 476 DIYOQLRNDSAEYKVGISWTDHLHLRTERMHWPQSGQQLPRISICSLPCQPCGERKKTGK 535  
QY 455 -----TIVTHVLR-----VSPLFLVC 471  
Db 536 MPCCWHCEPTGYQYQVDRTYCKTCPCYDMRPTENFTGCRPIPIIKLEMGSPWAVLPLFLA 595  
QY 472 MCTISSCGIFVAFALITFNINWKNHRRVIOSSHVPVNTIMLFGVILICISVILLGIDGRFV 531  
Db 596 VVGLAAT-LFWVITFVRN-----DTPIVKASGRELSYVILLAGIFLCYATFLM-----IA 645  
QY 532 SPEYPKICQARALLSTGFTLAYGAMFSKVMVRHRTTKAK--TDPKKKVEPKWLYTMV 589  
Db 646 EPD--LGTCSLRRRIFLGLGMSISYAALLTKTNRIYRIFEOGKRVSAPREFISPASQALIT 703

QY 590 SGLLSIDLIVLLSWQIFDPLQRYLETFFLEDVSTDDIKIRPELEHCEQSORSNMLGLIV 649  
Db 704 FSLISLQLLGLICVWFVVDVSHSVVD---FQD--QRTLPREFARGVVKCDI--SDLSLCL 756  
QY 650 YGKGLLIVRGLFLAYETRSIKVKQINDSRVVGMSIYNVVLCLITAPVGMVIAQQDAS 709  
Db 757 LGYSMLLMVCTVYVAIKTRGVP-ETFEAKPIGTMYTTCIVWLAFTPI--FFGTSQSD 813  
QY 710 FAFV-----ALAVIFCCFLSMILLIFVPKVIEWIRHPKAEKSKYNPDSAISKEDEERYOK 764  
Db 814 KLIYQTTTLTVSVLSASVSLGMLYMPKVYIILFHPQNVPKR-----KRSIK 861  
QY 765 LVTENEOLQRUITOK 779  
Db 862 AVVTAATMSNKFQK 876  
RESULT 13  
MGR7\_RAT ID MGR7\_RAT STANDARD; PRT; 915 AA.  
AC P35400;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE METABOTROPIC GLUTAMATE RECEPTOR 7 PRECURSOR.  
GN GRM7 OR GPRC1G OR MGLUR7.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=101116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;  
RX MEDLINE=94117433; PubMed=828585;  
RA Okamoto N., Hori S., Akazawa C., Hayashi Y., Shigemoto R.,  
Mizuno N., Nakanishi S.;  
RT "Molecular characterization of a new metabotropic glutamate receptor  
mGluR7 coupled to inhibitory cyclic AMP signal transduction.";  
RL J. Biol. Chem. 269:1231-1236(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Olfactory bulb;  
RX MEDLINE=94195260; PubMed=8145723;  
RA Saugstad J.A., Kinzie J.M., Mulvihill E.R., Segerson T.P.,  
Westbrook G.L.;  
RT "Cloning and expression of a new member of the L-2-amino-4-  
phosphonobutyric acid-sensitive class of metabotropic glutamate  
receptors.";  
RL Mol. Pharmacol. 45:367-372(1994).  
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR  
IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE  
ACTIVITY.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED THROUGHOUT THE BRAIN.  
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
CC STRONGEST, TO MGLUR4.  
CC  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; D16817; BAA04092.1; -  
CC EMBL; U06832; AAA20655.1; -  
CC GCRDB; GCR\_0945; -  
CC GCRDB; GCR\_0946; -  
CC InterPro; IPR001828; ANF\_receptor.  
CC InterPro; IPR000337; GPCR\_Mgr.  
CC Pfam; PF00003; 7tm\_3; 1.  
CC Pfam; PF01094; ANF\_receptor; 1.

DR PRINTS; PR00248; GPCRMR.  
 DR PRINTS; PR00593; MTABOTROPICR.  
 DR PRINTS; PR01057; MTABOTROPICR.  
 DR PROSITE; PS00979; G\_PROTEIN\_RECEP\_F3\_1; 1.  
 DR PROSITE; PS00980; G\_PROTEIN\_RECEP\_F3\_2; 1.  
 DR PROSITE; PS00981; G\_PROTEIN\_RECEP\_F3\_3; 1.  
 DR PROSITE; PS0259; G\_PROTEIN\_RECEP\_F3\_4; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 MW Multigene family; Olfaction.  
 FT SIGNAL 1 32 POTENTIAL.  
 FT CHAIN 33 915 METABOTROPIC GLUTAMATE RECEPTOR 7.  
 FT DOMAIN 33 590 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 591 615 I (POTENTIAL).  
 FT DOMAIN 616 627 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 628 648 II (POTENTIAL).  
 FT DOMAIN 649 654 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 655 675 III (POTENTIAL).  
 FT DOMAIN 676 702 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 703 723 IV (POTENTIAL).  
 FT DOMAIN 724 753 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 754 775 V (POTENTIAL).  
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 FT TRANSMEM 789 811 VI (POTENTIAL).  
 FT DOMAIN 811 825 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 826 850 VII (POTENTIAL).  
 FT DOMAIN 851 915 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 486 486 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 572 572 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 915 AA; 102231 MW; F28AFC4C6454A6C2 CRC64;

Query Match 8.1%; Score 353; DB 1; Length 915;  
 Best Local Similarity 21.2%; Pred. No. 5.2e-19;  
 Matches 206; Conservative 156; Mismatches 320; Indels 290; Gaps 50;

QY 17 LCLIA-----SPH-----LQGVAGRPDELHIGIPIAGKGGWQGOAC----- 57  
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 QY 58 ----MPATRLADVDNKNLPGFKL-----IL-----HSNDS 87  
 DB 75 GTHRLEAMLYALDQNSDNLNPNVTLGARILDCSDTYALEQSLTFVQALLQKDTSDV 134  
 QY 88 ECEPGLGASVMNLYNKPQKMLLAGC---STVCTTVAEAAKMNILVLCYGASSPALSD 145  
 DB 135 RCTNGEPP-----VFVKPEKVVGVIGASGSSVSMVANILRLFPQIPQISYASTAPELSD 188  
 QY 146 RKRFTPLFTHPSATVHNTRIKLKKFGNSRVAILQQAEEVFISVDELENRCMEAGVE 205  
 DB 189 DRYDFFSRVPPDSFQAQAMVDIVKALGN-----YVSTLAS-EGSYGEGKVE 236  
 QY 206 IYTRQSFSDPTDAVNLRL-----RODA-----RIIVGLFVVAARRVLC-----EMVKKQL 252  
 DB 237 SFTQISKEAGGLCIAGSVRIPOERKDRITDFDRIIKQLDTPNSRAVIFANEDIKQIL 296  
 QY 253 YG--RA--HVMFFIGWYEDNW-----YEVNKAEGITCTVEQMRAAEG---HLTTEAL 299  
 DB 297 AAAKRAQDVGHFLWVGSDSGSKINLQHEDIAEG-AITIQKRAVTEGFDAFTSRTL 355  
 QY 300 -----MW-----NONQTITISGMTAEF-RHRLNQALIEGYDINHRYPEGVQEAP 345  
 DB 356 ENNRNVWFAEYWEENFNCKLTISGSKEDTDKRCGQERI--GKDSNYEQ--EG--KVQ 409  
 QY 346 LAYDAVWSVALAFNKTMTERTLT-----GKKSILRDTFTYDKETADEIYAAMNS 392  
 DB 410 FVIDAVYAMAHALHNMKOLCADRYGVCPEMEQAGKKLLKYTRHVN----- 456  
 QY 393 TOFLGYSVG--VAFSSQGDRIALTQIBQMDIGKYEKLGYYDTQDLNLSW-----L 440  
 DB 457 --FNSAGTTPVFNKNGD-----APGRYDIFQYQTNTNTNPGYRLIGQWTDLQL 504

QY 441 NTE--QWIGG--KVQP-----DRTIVTH-- 459  
 DB 505 NIEDMQMGKGVREIPSSVCTLPCKPGQKTKQKTPCWTCEPCDGYQYQFDEMTQCHCP 564  
 QY 460 -----VLR-----VSLPLFVCMCTISSGIFVAFALIFINWNKRR 497  
 DB 565 YDQRPENRNTGCONIPIIKLEWHSPWAVIPVFLAMLGIAT-IFVMATFIRN----DTP 619  
 QY 498 VIOSSHPPVCFIMLFGVIICLISVILLGIDGRFVSPEYPKICQARAWLLSTGFTLAYGA 557  
 DB 620 IVRASGRELSYLLTGIFLCYIIFLM-----IAKPD--VAVCSFRVFLGLGMCISYAA 672  
 QY 558 MFSKWRVHRFTTKAK---TDPKKKVPKLYTMVSGLLSIDLVILLSWQIFDPLQRYLE 614  
 DB 673 LLTKNRIYRIFEGQKKSVTAP-RLISPTSLATSSLSVQLLGVIFWGVDPNIIID 731  
 QY 615 TFPLEDPVSTDDIKIRPELHESQSRNMMGLVYFGKLGILVFLGLFAYETRSIKVKQ 674  
 DB 732 ----YDEHKTMNPEQARGVLK-CDITDLQIICSL--GVSILLMVTCTVYAIKTRGVP-EN 783  
 QY 675 INDSRYGMSIYNNVVLCLITAPVGMVIAQOODASFAFV-----ALAVIFCCFLSMLLIF 729  
 DB 784 FNEAKPIGFTMYTTCIVMLAFIPI--FFGTAQSAEKLYIQTTTITISMNLSASVALGMLY 841  
 QY 730 VPKVIEVIRHPDKAESKYNPDSAISKEDEERYOKLVTENEQLORLITQKEEKIRVLQR 789  
 DB 842 MPKVIYIIFHPELVNQRR-----KNSFRAVTAATMSSRLSHKPSDR----- 883  
 QY 790 LVERGDAKGTTEL 801  
 DB 884 --PNGEAK--TEL 892

RESULT 14  
 MGR6\_RAT ID MGR6\_RAT STANDARD; PRT; 871 AA.  
 AC P35349;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE METABOTROPIC GLUTAMATE RECEPTOR 6 PRECURSOR.  
 GN GRM6 OR GPRC1F OR MGLUR6.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN NCBI\_TaxID=101116;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Retina;  
 RX MEDLINE=93280152; PubMed=8389366;  
 RA Nakajima Y., Iwakabe H., Akazawa C., Nawa H., Shigemoto R.,  
 RA Nakanishi S.;  
 RT "Molecular characterization of a novel retinal metabotropic glutamate  
 RT receptor mGluR6 with a high agonist selectivity for L-2-amino-4-  
 RT phosphonobutyrate";  
 RL J. Biol. Chem. 268:11868-11873(1993).  
 CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR  
 CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE  
 CC ACTIVITY.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: RESTRICTEDLY EXPRESSED IN THE INNER NUCLEAR  
 CC LAYER OF THE RETINA.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
 CC STRONGEST, TO MGLUR4.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC

DR EMBL: D13963; BAA03066.1; --  
DR PIR: A46742; A46742.  
DR GCRdb; GCR\_0623; --  
DR InterPro; IPR001828; ANF\_receptor.  
DR InterPro; IPR000337; GPCR\_Mgr.  
DR Pfam; PF00003; 7tm.3; 1.  
DR Pfam; PF01094; ANF\_receptor; 1.  
DR PRINTS; PR00248; GPCR\_MGR.  
DR PRINTS; PR00593; MTABOTROPICR.  
DR PRINTS; PR01056; MTABOTROPICR.  
DR PROSITE; PS00979; G\_PROTEIN\_RECEP\_F3\_1; 1.  
DR PROSITE; PS00980; G\_PROTEIN\_RECEP\_F3\_2; 1.  
DR PROSITE; PS00981; G\_PROTEIN\_RECEP\_F3\_3; 1.  
DR PROSITE; PS0259; G\_PROTEIN\_RECEP\_F3\_4; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
KW Multigene family; Vision.  
FT SIGNAL 1 18  
FT CHAIN 19 871  
FT DOMAIN 19 579  
FT TRANSMEM 580 602  
FT DOMAIN 603 616  
FT TRANSMEM 617 637  
FT DOMAIN 638 648  
FT TRANSMEM 649 667  
FT DOMAIN 668 691  
FT TRANSMEM 692 712  
FT DOMAIN 713 742  
FT TRANSMEM 743 764  
FT DOMAIN 765 777  
FT TRANSMEM 778 800  
FT DOMAIN 801 813  
FT TRANSMEM 814 839  
FT DOMAIN 840 871  
FT CARBOHYD 290 290  
FT CARBOHYD 445 445  
FT CARBOHYD 473 473  
FT CARBOHYD 561 561  
SQ SEQUENCE 871 AA; 95089 MW; 9F70B4D6A13B186D CRC64;  
  
Query Match 7.6%; Score 334.5; DB 1; Length 871;  
Best Local Similarity 20.3%; Pred. No. 1.3e-17;  
Matches 180; Conservative 158; Mismatches 350; Indels 199; Gaps 39;  
  
QY 11 VTFWIF---LCLLTASPHLOGVAGRPDELHIGGIFPIAGKGGWGGQAC-----57  
Db 11 LAWLISQAGIACGAGSVRLAGG-----LTIGLFPVHARGA--AGRACGALKKEQGVH 61  
  
QY 58 -MPATRLALDDVKNQPLLPGLKILHNSDECE-----PGLGA 95  
Db 62 RLEAMLYALDRVNDAPPELLPGVRLGARLLDT-CSDRTYALQALSFVQALLNGRGDGEA 120  
  
QY 96 SV-----MYNLLYNKPKMLLAG--CSTVCTTVAEAKMNLIVLCYGASSPALSDRRK 148  
Db 121 SVRCPGGVPLRSAPPRVAVVAVGASASSVIMVANVRLFAIPQISYASTAPELSDSTR 180  
  
QY 149 FPLTFRTHPATVNPRIKLMKFGSRVAIL-----QQAEEVFSTVEDLENRME 201  
Db 181 YDFSRVVPDPSYQAQAMVDIVRALGWNVYSTLASSENGYSGEAFVQISREAGGVGIA 240  
  
QY 202 AGVEIVTRQSLSDPTDAVRNLRR---QDARIIVGLFVYVAARVLCVMYKQQLYGRAH 257  
Db 241 QSIKIPREPCK---PGEHKVIRRLMETPNARGIIIFANEDDIRKVLATQANLTGH-- 294  
  
QY 258 VWFFIGWYEDNWE-----VNLKAEGI-TCTVEQMRIAAEG---HLTTEALMWNNOHTT 308  
Db 295 -FLAVG--SDSWGSKISPLNLEEAVGAILPKRASIDGFDQYFMRSL---ENNRN 348  
  
QY 309 ISGMTAEFRHLNQAIEGID-----INHDYRPEGYQAPLAYDAVWSVA 355  
Db 349 I--WFAEFWEENFNKLTSSGGQSDSTRKCTGEEIRGQDSAYEQEGKVQFVIDAVYAIA 406  
  
QY 356 LAFNKTWERLITGKSL-RDFTYTDKETADEIYAAMNSTQFLGVSGV-VAFSSQGD---R 410

Db 407 HALHSMHQALCPGHTGLCPANEPTD---GRTLLHYIARVFNCSAGTPVFNENGDPGR 463  
QY 411 IALTQIE---QMIDGKYEKLGY--DTQLDNLNLSWLNTEQWIGG--KVPODRITV----- 457  
Db 464 YDIFQYQATNGSASSGGYQAVGQWAEALRD---MEVLRWSGDPHEVPSQCSLPCGPG 519  
QY 458 -----THVLR-TVSLPL 468  
Db 520 ERKKMKVGPCCWHCEACDGYRFQVDEFTCEACPGDMRPTNHTGCRPTVVRLTWSSPW 579  
QY 469 FVCMCTISSCGIFVAFALIIFNKNHRRVIOSSHPCVNTIMLFGV-IICLISVILLGID 527  
Db 580 AALPLLLAVLGINATTIMATFMRHNDTPIVRASGRSLSYLLTGLTFLIYAITFLMYA-- 637  
QY 528 GREVSPPEYPKICQARAWLLSTGTTLAYGAMFSKVRVHRFTTKAK--TPKKKVEPWKL 585  
Db 638 -----EPCAAIACAARRLLGLTGLTSLYSALLTKTRIYRIFEGQKRSTVPPFISPTSQ 691  
QY 586 YTMVSGLLSIDLVILLSWQIFDPLQRYLETFFLEDVPTTDDIKRPELHESQSRNSMW 645  
Db 692 LVITEGLTSLQVVGVIANLGAQPPHSHVID---YEQRVTVDPEQARGVLA-CDMSDLSL- 745  
QY 646 LGLVYGFGLILVFLGFLAYETRSIKVKQINDSRVYGMISYINVVVLCILITAPVGMVJASQ 705  
Db 746 IGLL-GYSLILMVTCTVYAIKARGVP-ETFEAKPIGFTMYTTCIIWLAFVPI--FFGTA 801  
QY 706 QDASFAPV-----ALAVIFCCFLSMLLIFVPKIVIEIRHPKDKAESK 747  
Db 802 QSAEKIYIOTTLTVLSLSASVSLGMLYVPKTYVILFHPQNVQKR 848  
  
RESULT 15  
MGR3\_RAT  
ID MGR3\_RAT STANDARD; PRT; 879 AA.  
AC P31422;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE METABOTROPIC GLUTAMATE RECEPTOR 3 PRECURSOR.  
GN GRM3 OR GPRC1C OR MGLUR3.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=92110002; PubMed=1309649;  
RT Tanabe Y., Masu M., Ishii T., Shigemoto R., Nakanishi S.;  
RT "A family of metabotropic glutamate receptors."  
RL Neuron 8:169-179(1992).  
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR  
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE  
CC ACTIVITY.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -!- TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS. PREDOMINANT  
CC EXPRESSION IS SEEN IN THE NEURONAL CELLS OF THE CEREBRAL CORTEX,  
CC DENTATE GYRUS, AND GLIAL CELLS THROUGHOUT BRAIN REGIONS.  
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
CC STRONGEST, TO MGLUR2.  
  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; M92076; -; NOT\_ANNOTATED\_CDS.  
DR PIR: JH0562; JH0562.  
DR GCRdb; GCR\_0362; -;

DR InterPro; IPR001828; ANF\_receptor.  
DR InterPro; IPR000337; GPCR\_Mgr.  
DR Pfam; PF00003; 7tm\_3; 1.  
DR Pfam; PF01094; ANF\_receptor; 1.  
DR PRINTS; PR00248; GPCRMR.  
DR PRINTS; PR01053; MTABOTROPIC3.  
DR PROSITE; PS00979; G\_PROTEIN\_RECEP\_F3\_1; 1.  
DR PROSITE; PS00980; G\_PROTEIN\_RECEP\_F3\_2; 1.  
DR PROSITE; PS00981; G\_PROTEIN\_RECEP\_F3\_3; 1.  
DR PROSITE; PS00982; G\_PROTEIN\_RECEP\_F3\_4; 1.  
DR PROSITE; PS0259; G\_PROTEIN\_RECEP\_F3\_4; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
KW Multigene family.  
FT SIGNAL 1 22  
FT CHAIN 23 879  
FT DOMAIN 23 576  
FT TRANSMEM 577 599  
FT DOMAIN 600 613  
FT TRANSMEM 614 634  
FT DOMAIN 635 645  
FT TRANSMEM 646 664  
FT DOMAIN 665 688  
FT TRANSMEM 689 709  
FT DOMAIN 710 734  
FT TRANSMEM 735 756  
FT DOMAIN 757 769  
FT TRANSMEM 770 792  
FT DOMAIN 793 802  
FT TRANSMEM 803 828  
FT DOMAIN 829 879  
FT CARBOHYD 209 209  
FT CARBOHYD 292 292  
FT CARBOHYD 414 414  
FT CARBOHYD 439 439  
SQ SEQUENCE 879 AA; 98959 MW; 3E5965EDD5E6DEED CRC64;

Query Match 7.6%; Score 333; DB 1; Length 879;  
Best Local Similarity 20.6%; Pred. No. 1.7e-17;  
Matches 180; Conservative 132; Mismatches 313; Indels 250; Gaps 39;

Qy 36 ELHIGGIFPIAGKGGWQGC-----MPATRALDQVKNOPNLLPGFKLILHS 84  
Db 38 DLVLGLFPINERG--TGTECGRINEDRGIQRLAFLFAIDINKDNYLLPGVKGVHI 95  
Qy 85 NDS-----ECPGLGASVMYNNLYNKPCKMLLAGC-- 115  
Db 96 LQTCSDTYALQSLFVFRASLTQVDEAYMCPDG-----SYAIQENIP---LLIAGVIG 147  
Qy 116 ----STVCTTVAEAKMNNILVLCYGASSPALSQRKPTFLTHPSATVHNPTRIKMK 172  
Db 148 GSYSSVSIQVALLRLFLQIPQISYASTSAKLSKSDRYDYFARTVPPDFYQAKAMAEILRF 207  
Qy 173 FGWSRVAILQQAEEVFISTVELE-----NRCMEAGVEIVTROSFLSDPTDAVRN-LRR 225  
Db 208 FNWTYVSTVASEGDYGETGIEAFQEARLNICI-ATAEKVGRSNIRKSYDSVIRELLQK 266  
Qy 226 QDARIIVGLF-----YVVAARRVLCEMYKOOLYGRAHVWFEEIGWYEDNNYEVNLKAE 277  
Db 267 PNARVVV-LFMRSDSDSRELIAANRV-----NASFTWV-----ASDGWG-----AOE 307  
Qy 278 GITCTVEOMRIAAEGHLLTTEAL-----MNNQNNQTTIS 310  
Db 308 SI--VKGSEHVAYGAILLELASHPVQDRFYQSLNPNYNNHRNPWFDFEOKFQCSLQ 364  
Qy 311 GMTAEERHRLNQALIEGYDINHDPYEGYQAPLAY--DAVMSVALAFNKTMERLTGT 368  
Db 365 -----NKRNRHOCVCKHLAIDSNEY--QESKIMFVVNAVYAMAHALKMORTLCPN 414  
Qy 369 KKSRLDF--TYTDKETADEIYAMNSTQFL-----GVSGVVAFSSQGDRIALTQI--EQMI 420  
Db 415 TTKLCDAMKILDGKLYKEYLLKINFTAPFPNPKGADSIKFDFTFGDGMGRYVNFNLQOT 474

. . . . .

Qy 421 DGKYE--KLGYY----DTQLDNLQSW----LNTQ-----WI----- 446  
Db 475 GGRYSYLKVGHWAEITSLDVSIIHWSRNSVPTSCSDPCAPNEMKNMQPGDVCCWICIPC 534  
Qy 447 -----GKVP-----QDRTIIVTHVLRVTSPLFVCMC 473  
Db 535 EPEYLVDEFTCMDCGPGOWTADLSGCYNLPEDYIKWEDAWAIGPV--TIACLGFLCTC 592  
Qy 474 TISSCGIFVAFALIFINWKNHRR---VIOSSHVPVCNTIMLFGVIICLISVILLGIDGRF 530  
Db 593 -----IVITVFIKHNNTPLVKASGRELC-YILLFGVSLSYCMTF-----F 631  
Qy 531 VSPPEYKICQARAWILLSTGTLAYGAMFSKVRVHRTTAKTDPK--KKVEPKLYTM 588  
Db 632 FIAKPSPVICALRRLLGLTSAICYALLTKTNCIARIFDGVKNGAQRPKFISPSQVFI 691  
Qy 589 VSGLLSIDLVILLQWQIFDP--LQRYLETFFLEDVSTDDIKIRPELEHCEESRNSMWL 646  
Db 692 CLGLILQIVMVSVWLLILETPTTRY--TLP-----EKRETVILKCNVDSSMLI 739  
Qy 647 GLVYGFKGLILVFLGLLAYETRSIKVKOINDSRVYGMISYNNVVLCLITAPVGMVIAQQ 706  
Db 740 SLTYDV--VLVILCTVYAFKTRKCP-ENFNEAKFIGFTMYTTCIIWLAFLEPFIYVVTSSDY 796  
Qy 707 DASFAFVALAVIFCCFLSMLLIFVPKVIETVIRHPK 741  
Db 797 RVQTTMCISVSLSGFVVVLGCLFAPKVHIVLFQPO 831

Search completed: April 30, 2002, 10:16:52  
Job time: 224 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:12:33 ; Search time 32.13 Seconds  
(without alignments)  
3824.113 Million cell updates/sec

Title: US-09-715-962-2  
Perfect score: 4374  
Sequence: 1 MKKDMTSDGAVTFWIFLLCL.....LINSSAHATPAATLAITQGE 840

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL\_17.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4374	100.0	840	5 Q9BML7	Q9bml7 drosophila
2	3317	75.8	1713	5 Q9V309	Q9v3q9 drosophila
3	1746	5	39.9	5 Q9N502	Q9n502 caenorhabdi
4	1186	5	27.1	5 Q9BML6	Q9bml6 drosophila
5	1183	5	1221	5 Q9Y133	Q9yl33 drosophila
6	1022	5	23.4	5 Q9VPS7	Q9vps7 drosophila
7	1018	5	23.3	5 Q9BML5	Q9bml5 drosophila
8	457	10.4	402	5 Q23442	Q23442 caenorhabdi
9	362	5	8.3	5 Q9V485	Q9v485 drosophila
10	343	5	7.9	11 Q62916	Q62916 rattus norv
11	342	7.8	879	11 Q9QYS2	Q9qys2 mus musculu
12	334	5	7.6	5 Q9G954	Q9g954 geodia cydo
13	330	7.5	872	4 Q9H3N6	Q9h3n6 homo sapien
14	330	7.5	977	13 Q9PWE1	Q9pwe1 ictalurus p
15	299	5	6.8	1188 13 Q9BUC5	Q9buc5 gallus gall
16	297	5	6.8	1242 13 Q9BUC4	Q9buc4 gallus gall
17	294	5	6.7	1156 13 Q9BUC6	Q9buc6 gallus gall
18	274	5	6.3	153 11 Q9QY85	Q9qy85 rattus norv
19	267	6.1	1199	11 Q9EPV6	Q9epv6 mus musculu

20	247.5	5.7	870	5 Q9M4T8	Q9m4t8 caenorhabdi
21	243.5	5.6	856	13 Q73638	Q73638 fugu rubrip
22	241.5	5.5	868	13 Q73636	Q73636 fugu rubrip
23	240	5.5	912	10 Q9C561	Q9c561 arabidopsis
24	237	5.4	877	13 Q9PW88	Q9pw88 carassius a
25	235	5.4	844	13 Q93552	Q93552 carassius a
26	231.5	5.3	738	5 Q9V4U3	Q9v4u3 drosophila
27	231.5	5.3	864	13 Q73637	Q73637 fugu rubrip
28	227	5.2	875	13 Q73640	Q73640 fugu rubrip
29	224.5	5.1	1056	13 Q9Y117	Q9y117 squalus aca
30	223	5.1	1055	13 Q9YGM3	Q9ygm3 oryzias lat
31	222	5.1	1055	13 Q98U11	Q98u11 oryzias lat
32	219.5	5.0	848	13 Q93553	Q93553 carassius a
33	219	5.0	941	10 Q9SWD9	Q9swd9 arabidopsis
34	212	4.8	1267	5 Q93564	Q93564 caenorhabdi
35	211.5	4.8	925	10 Q65498	Q65498 arabidopsis
36	211.5	4.8	962	10 Q23048	Q23048 arabidopsis
37	209	4.8	1070	13 Q93490	Q93490 anguilla ja
38	207	4.7	808	11 Q35190	Q35190 mus musculu
39	202.5	4.6	880	13 Q73639	Q73639 fugu rubrip
40	201.5	4.6	912	10 Q9SES5	Q9ses5 brassica na
41	195	4.5	843	11 Q9Z0R7	Q9z0r7 rattus norv
42	193.5	4.4	551	13 Q9PWQ0	Q9pwq0 fugu rubrip
43	190.5	4.4	923	10 Q9ZV68	Q9zv68 arabidopsis
44	189.5	4.3	953	10 Q9ZV67	Q9zv67 arabidopsis
45	187	4.3	502	13 Q98845	Q98845 anguilla ja

#### ALIGNMENTS

RESULT 1  
Q9BML7 PRELIMINARY; PRT; 840 AA.  
ID Q9BML7;  
AC Q9BML7;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE METABOTROPIC GABA-B RECEPTOR SUBTYPE 1.  
GN GABA-B-R1.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=11168554;  
RA Mezler M., Muller T., Raming K.;  
RT "Cloning and functional expression of GABA-B receptors from  
RT Drosophila.";  
RL Eur. J. Neurosci. 13:477-486(2001).  
DR EMBL; AF318272; AAK13420.1; -.  
KW Receptor.  
SQ SEQUENCE 840 AA; 94384 MW; C091A9F406C97500 CRC64;

Query Match 100.0%; Score 4374; DB 5; Length 840;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRKDMTSDGAVTFWIFLLCLIASPHLQGGVAGRPDELHIGGIFPIAGKGWGGQACMPA	60
DB	1	MRKDMTSDGAVTFWIFLLCLIASPHLQGGVAGRPDELHIGGIFPIAGKGWGGQACMPA	60
QY	61	TRLALDDVKNQPNLLPGFKLILHSNDSECEPGLGASVMYNLLYNKPKMLLAGCSTVCT	120
DB	61	TRLALDDVKNQPNLLPGFKLILHSNDSECEPGLGASVMYNLLYNKPKMLLAGCSTVCT	120
QY	121	TVAEAAKMNNLIVLCYGASSPALSDDRPFPTLFRTHTPSATVHNPTRIKLMKKGWSRVAI	180
DB	121	TVAEAAKMNNLIVLCYGASSPALSDDRPFPTLFRTHTPSATVHNPTRIKLMKKGWSRVAI	180

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OY 181 LQAAEEVFISTVEDLENRCMEAGVEIVTRQSFSLSDPTDAVRNLRRODARIIVGLFVWAA 240
DB 181 LQAAEEVFISTVEDLENRCMEAGVEIVTRQSFSLSDPTDAVRNLRRODARIIVGLFVWAA 240
OY 241 RRVLCENTYKQQLYGRAHVFFIIGWYEDNNYEVNKAEGITCTVQEOMRIAAEGHLLTTEALM 300
DB 241 RRVLCENTYKQQLYGRAHVFFIIGWYEDNNYEVNKAEGITCTVQEOMRIAAEGHLLTTEALM 300
OY 301 WNQNQTTISGMTAEFRHRLNQALIEEGYDINHDPYRPGYQAPLAYDAVWSVALAFNK 360
DB 301 WNQNQTTISGMTAEFRHRLNQALIEEGYDINHDPYRPGYQAPLAYDAVWSVALAFNK 360
OY 361 TMRUFTTGKSLRDFTYTDKETADEIYAAMNSTOFLGVSQVAFSSQDGRALQTLEQMI 420
DB 361 TMRUFTTGKSLRDFTYTDKETADEIYAAMNSTOFLGVSQVAFSSQDGRALQTLEQMI 420
OY 421 DGKYEKLGYYDQDLNLSWLNTQEWIGGKVPQDRTIVTHVLRVSLPLFVCMCTISSCGI 480
DB 421 DGKYEKLGYYDQDLNLSWLNTQEWIGGKVPQDRTIVTHVLRVSLPLFVCMCTISSCGI 480
OY 481 FVAFALLIPIFNKRRVTOSSHPVQNTIMLFGVILCLISVILLGIDGRVSPPEEYPKIC 540
DB 481 FVAFALLIPIFNKRRVTOSSHPVQNTIMLFGVILCLISVILLGIDGRVSPPEEYPKIC 540
OY 541 QARAWLLSGFTFLAYGAMESKYVRVHRFTTKAKTDPKKKVPEPKLYTMVSGLLSIDLVIL 600
DB 541 QARAWLLSGFTFLAYGAMESKYVRVHRFTTKAKTDPKKKVPEPKLYTMVSGLLSIDLVIL 600
OY 601 LSWQIFDPLQRYLETFPLPDDPVSTDDIKIRPELEHCEQSORSNWMGLVYGFGLILVFG 660
DB 601 LSWQIFDPLQRYLETFPLPDDPVSTDDIKIRPELEHCEQSORSNWMGLVYGFGLILVFG 660
OY 661 LFLAYETRSIKVKQINDSRVGMISYNNVVLCLITAPVGMVIAOQDASFAFVALAVIFC 720
DB 661 LFLAYETRSIKVKQINDSRVGMISYNNVVLCLITAPVGMVIAOQDASFAFVALAVIFC 720
OY 721 CFLSMILLIFPVKVIEWIRHPKKAESKYNPDSAISKEDEERYOKLTENBQLRLTQKE 780
DB 721 CFLSMILLIFPVKVIEWIRHPKKAESKYNPDSAISKEDEERYOKLTENBQLRLTQKE 780
OY 781 EKIRVLQRQLVERGDAKGPENLNGATGVASAAVATTQSPASLINSSAHATPAATLATOGE 840
DB 781 EKIRVLQRQLVERGDAKGPENLNGATGVASAAVATTQSPASLINSSAHATPAATLATOGE 840

RESULT 2
OY 09V309 PRELIMINARY; PRT: 1713 AA.
AC 09V309;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CG15274 PROTEIN.
CN GABA-B-R1 OR BG:DS00929.6 OR CG15274.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
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RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cusley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gong F., Gong F., Garret J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Glodek A., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei V., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulo G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Y, AND CN BW SP;
RX MEDLINE=99403001; PubMed=10471707;
RA Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
RA Celniker S., Rubin G.M.;
RT "An exploration of the sequence of a 2.9-Mb region of the genome of
RT Drosophila melanogaster: the Adh region."
RL Genetics 153:179-219(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-Y, AND CN BW SP;
RA Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
RA Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lonotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zieran L.L., Rubin G.M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003646; AAF53431.1; -
DR EMBL; AE003411; AAF44910.1; -
DR FlyBase; FBgn0028924; GABA-B-R1.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR000402; Na_K_beta.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF00287; Na_K-ATPase; 1.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 2.
KW Hypothetical protein.
SQ SEQUENCE 1713 AA; 195133 MW; 8474EBC5F9FA27AC CRC64;
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Query Match 75.8%; Score 3317; DB 5; Length 1713;
Best Local Similarity 45.0%; Pred. No. 7.3e-251;
Matches 737; Conservative 16; Mismatches 19; Indels 866; Gaps 10;

OY 3 KDMTSDGAVTFWIFLLCLIASPHLQGGVAGRPDELHIGGIFPIAGKGGQGGQACMPATR 62
DB 142 RDMTSDGAVTFWIFLLCLIASPHLQGGVAGRPDELHIGGIFPIAGKGGQGGQACMPAAR 201
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Qy	63	LALDDVNKQPNLLPGFKLLIHSNDSCEPGLGASVYNNLLYNPKQKMLMLLAGCSTVCTTV	122
Db	202	LALDDVNKQPNLLPGFKLLIHSNDSCEPGLGASVYNNLLYNPKQKMLMLLAGCSTVCTTV	261
Qy	123	AEAAKWNLLIVLCYGASSPALSDRKFPPTLFRTHPSATVHNPTRIKLMKFGSRVAILQ	182
Db	262	AEAAKWNLLIVLCYGASSPALSDRKFPPTLFRTHPSATVHNPTRIKLMKFGSRVAILQ	321
Qy	183	QAEVFI STVEDLENRCMEAGVEIVTRQSFSDPTDAVNLRRQDARIIVGLFVVAARR	242
Db	322	QAEVFI STVEDLENRCMEAGVEIVTRQSFSDPTDAVNLRRQDARIIVGLFVVAARR	381
Qy	243	VLCEMYKOOLYGRAHWFFIGWYEDNWYEVNLUKAEGITCTVEQMRTAAEGHLTTEALMWN	302
Db	382	VLCEMYKOOLYGRAHWFFIGWYEDNWYEVNLUKAEGITCTVEQMRTAAEGHLTTEALMWN	441
Qy	303	QNNQTTISGMTAEFF-----RHRLNQALIEEGYDINHDNRPEGY	341
Db	442	QNNQTTISGMTAEERLVLLVPLKFLQCAFFLRHRLNQALIEEGYDINHDNRPEGY	501
Qy	342	QEAPLAYDAVWSVALAFNKTMERLATGKKSRLDFTYTDKEIADEIYAAMNSTOFLGVSGV	401
Db	502	QEAPLAYDAVWSVALAFNKTMERLATGKKSRLDFTYTDKEIADEIYAAMNSTOFLGVSGV	561
Qy	402	VAFSSQGRIALTQIEQMTIDGKYKELGYDYDTOLDNISWLNTEQWIGK-----	449
Db	562	VAFSSQGRIALTQIEQMTIDGKYKELGYDYDTOLDNISWLNTEQWIGKKTTHVTEPNKN	621
Qy	450	-----VPO-----	449
Db	622	GNPSKDDVNTRGSLTSLSEKNDSEKNPSSASLQQAQKVPAPKPKKLSISDAGKDTVTQKV	681
Qy	450	-----	449
Db	682	KENEPGSKQEKESIGVYRANRNSATKKEKLLVKTVPGKSLIKESNDENVEPSRRT	741
Qy	450	-----	449
Db	742	KSQPVGKKVYESTRRVREPFDSPDREXYLSDMIDYDRSDEDVPEKKLSWEPDSTLRRR	801
Qy	450	-----VPO-----	452
Db	802	FVSNNEYHSLGEBEEIDLDSVGSMTRGSYRMPQNAEDERPVI LAEIIINMKGLKELKE	861
Qy	453	-----DRTI-----VTHV-----VTHV-----	460
Db	862	QRESTNVFNRRDOKTIDEVGSKITGTYSKQHVEVKYNETASNEDDDNAQVKHIGTIT	921
Qy	461	-----	460
Db	922	KIFSAQRMKEKKSESEDENKDENVKDKENKDDQKLPPEPEIELEAKKAWTFPI	981
Qy	461	-----	460
Db	982	AETSPDIPGQNILOEYQVKYIGKRNRYRCIGINTDISRKSXIKTFISKAGDGLVYH	1041
Qy	461	-----LRTVSLPLFV-----	470
Db	1042	DGGRLEDIGOTTENLKNQRKNHKKTEPPDIPVDIGHSDDRVREIGVNTKKLPRIIPPI	1101
Qy	471	-----	470
Db	1102	AEHVHKNGLRDICTSTDKPFPIDDDGTDVYMHPIKTRDKKLNKLIVDPDPDNGPYKM	1161
Qy	471	-----C-----MCTISSCGIFVAFALII	488
Db	1162	PTKEDRRTYYKGEYHFPGTREWRLFNKIHGKYKLRRP SHWLYTLVFSVLYILFWIIF	1221
Qy	489	FNW-----	492
Db	1222	SWANPDFIKDDASRKVPIMKMAQPFISFTPIGRTNPKAVSFDPNRNSTEYMEKYAGIMAL	1281

Qy	493	-----	-----	492	
Db	1282	LEKYGDYGHNP	RGCTCANKEKFGYSPGCEPCVFLKVNRIIGFKTEPYINSDELVRKAKIDEV	1341	
Qy	493	-----	-----N 493	-----	
Db	1342	EFTALKLLENTTTEGHLNRTWITCRSDKDKNKLIEFHPPEPAITEYTDIEEKLEYIAN	1401		
Qy	494	KHRR	-----VIQSSHPVCNTIMLFGVVIICLISVI	522	
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Db	1402	EGKKSFFGPN	VNRIVALIKNLKANERVHINCKIVIQSSHPVCNTIMLFGVVIICLISVI	1461	
Qy	523	LLGIDGRFVSPEEY	PKICQARAWLLSTGFTLAYGAMFSKWKVRHRTTKAKATDPKKKVEP	582	
	:	:			
Db	1462	LLGIDGRFVSPEEY	PK	1477	
Qy	583	WKLYTWYSGLLS	IDLVLLSQWIFDLPORYLETFPLEDPVSTTDDIKIRPELEHCE	SO	642
Db	1478	-----	-----IFDPLQRYLETFPLEDPVSTTDDIKIRPELEHCE	SO	1515
Qy	643	SMWGLGVYGF	KGLILVFLGFLAYETRSIKVKQINDSRVYGMSIYNVVVLC	LITAPVGMVI	702
	:	:			
Db	1516	SMWGLGVYGF	KGLILVFLGFLAYETRSIKVKQINDSRVYGMSIYNVVVLC	LITAPVGMVI	1575
Qy	703	ASQODASFAF	VALAVIFCCFLSMILLIFVPKVIETVIRHPKDKAESKYNPDS	SAISDEDERY	762
	:	:			
Db	1576	ASQODASFAF	VALAVIFCCFLSMILLIFVPKVIETVIRHPKDKAESKYNPDS	SAISDEDERY	1635
Qy	763	OKLTENEOLQ	RLITQEEKIRVRLORLVERGDAGKTELGATGVSAAVATT	SOPASLI	822
	:	:			
Db	1636	OKLTENEOLQ	RLITQEEKIRVRLORLVERGDAGKTELGATGVSAAVATT	SOPASLI	1695
Qy	823	NSSAHATPAAT	LAITQGE	840	
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Db	1696	NSSAHATPAAT	LAITQGE	1713	
RESULT	3				
Q9N502					
ID	Q9N502	PRELIMINARY;	PRT;	816 AA.	
AC	Q9N502;				
DT	01-OCT-2000	(TReMBLrel. 15, Created)			
DT	01-OCT-2000	(TReMBLrel. 15, Last sequence update)			
DT	01-JUN-2001	(TReMBLrel. 17, Last annotation update)			
DE	Y41G9A.4	PROTEIN.			
DE	Y41G9A.4				
OS	Caenorhabditis elegans.				
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;				
OC	Rhabditidae; Pelodierinae; Caenorhabditis.				
OX	NCBI_TaxID=6239;				
RN	[1]				
RC	SEQUENCE FROM N.A.				
RC	STRAIN-BRISTOL N2;				
RX	MEDLINE=99069613; PubMed=9851916;				
RA	None;				
RT	"Genome sequence of the nematode C. elegans: a platform for				
RT	investigating biology. The C. elegans Sequencing Consortium.";				
RL	Science 282:2012-2018(1998).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-BRISTOL N2;				
RC	STRAIN-BRISTOL N2;				
RA	Waterston R.;				
RT	"The sequence of C. elegans cosmid Y41G9A.";				
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-BRISTOL N2;				
RC	STRAIN-BRISTOL N2;				
RA	Waterston R.;				
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AC006761; AAF60549.1; -;				
DR	InterPro; IPR001828; ANF_receptor.				
DR	InterPro; IPR000337; GPCR_Mgr.				
DR	Pfam; PF00003; 7tm3; 1.				





Db 759 FRKALMEKENELQALIRKL---GPEARKWIDGVTCTGGSNVSGSELEP 802

RESULT 5

Q9Y133 ID Q9Y133 PRELIMINARY; PRT; 1221 AA.

AC Q9Y133

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE BCDA:GH07312 PROTEIN.

GN GABA-B R2 OR BCDA:GH07312 OR CG6706.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Anantides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,

RA Folsler C., Gabrielian A.C., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Munkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-F., Wassarman D.A., Weinstock G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster."

RL Science 287:2185-2195(2000).

RN [2]

RP SEQUENCE FROM N.A.

RA Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G.,

RA Agbayani A., Arcalia T.T., Baxter E., Blazej R.G., Butenhoff C.,

RA Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E.,

RA Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,

RA Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M.,

RA Park S., Sequeira A., Sethi H., Snir E., Svirskaas R.R., Weinburg T.,

RA Celniker S.E.

RT "Full length Drosophila melanogaster cDNA sequence."

RL Submitted (Apr-1999) to the EMBL/genBank/DBJ databases.

DR EMBL; AE003736; AAF55916.1; -

DR EMBL; AF145639; AAD38614.1; -

DR FlyBase; FBgn0027575; GABA-B R2.

DR InterPro; IPR001828; ANF\_receptor.

DR InterPro; IPR000337; GPCR\_Mgr.

DR Pfam; PF00003; 7tm\_3; 1.

DR Pfam; PF01094; ANF\_receptor; 2.

DR PROSITE; PS02059; G\_PROTEIN\_RECEP\_F3\_4; 1.

SQ SEQUENCE 1221 AA; 138123 MW; A57A9954F31F0A05 CRC64;

Query Match 27.1%; Score 1183.5; DB 5; Length 1221;

Best Local Similarity 32.8%; Pred. No. 9.9e-84;

Matches 271; Conservative 184; Mismatches 311; Indels 61; Gaps 23;

QY 17 LLCLIASPHLOQGVAGRPDELHIGGIPPIA-GKGGWGGQACHPATPRLALDDVKNQPNLL 75

DB 12 LFLLELLWSTACGTAKRSD-VYTAGFFYGDGVENSYTGKVPMSVKVLAIGHVNEHGKL 70

QY 76 PGFKLILHSNDSCEPCGLGASVMYLNLYNKPOKMLL-AGCSTVCTTVAEAAKWNLI 134

DB 71 ANYRLHWNNDTCNNAAGVGVKSFDDMMHSGPNKVMLEGAACHTVTDPIAKASHWHLTQL 130

QY 135 CYGASSPALSDRRKRPFTLFTHPSATVHNTRIKLMKFGWSRVAILQQAEEVFI----S 190

DB 131 SYADTHPMET-KDAFPNFRVPSENAFNAPRLALLKEFNTRVGTVYQNEPRYSLPHNH 189

QY 191 TVEDLENRCMEAGVEIVTROSFLSDPTDAVNRNRQDARIIVGLFYVVAARRVCEMYKQ 250

DB 190 MVADLD--AME--VEVETQSFVNDVAESLKLREKDVRIILGNFNEHFARKAFCEAYKL 245

QY 251 QLYGRAHVWFFIGWYEDNWVEVNLKAGITCTVEQMRIRAAEGHLLTTEALWNNONNQTIS 310

DB 246 DMVGRAYQLIMATYSTDMWNVTDQSE---CSVEEIIATALEGAILVDLLPLSTSGDITVA 302

QY 311 GMTAEFRRLNQLAIEEYD---INHRYRPGYQAPLAYDAVMSVALAFNKTMRILT 366

DB 303 GITADEY-----LYE--YDRLGTEYSRF-HGY-----TYDGIWAAALAIQYVAEK-- 345

QY 367 TGKSLRDFTYTDKEIADEIYAAMNSTQFLGVSGWVAFFSQGDRIALTQIEQMDIGKYEK 426

DB 346 -REDLLTHEDYRVKDWESVLEALRNTSFGVTGPVRFYN-NERKANILINQFOLGQMEK 403

QY 427 LGYDITOLD--NLSWLNTEQWIGKVPQDRTIVTHVLTSLPLFCVMCTISSCGIFVAF 484

DB 404 IGEYHSQKSHLDLSLGPVKWVGKTPKDRTLIYIEHSQYNPTIYIVSASVIGVLIAT 463

QY 485 ALLIENIWNKHRRVIOSSHPCVNTIMLFGVILICISVILLIGIDGRFVSPPEYKICQARA 544

DB 464 VFLAFNIKYRNQRIYIKMSSPHLNLIIVGCMMYLSLIIFLGDLTTLSSVAAPFYICTARA 523

QY 545 WLLSTGFTLAYGAMFSKVMRVHRTTKAKTDPKKVPWKLYTMVSGLLSIDLVILLSWQ 604

DB 524 WILMAGFSLSPGAMFSKTRVHSHFTDLKLN-KKVIKDYQLFMVGVLLAIDAIITWQ 582

QY 605 IFDPLQRYLETFFLEDPV--STTDDDKIRPELEHESQORNMMGLVYGFGLILVFGLF 662

DB 583 IADPF--YRETKQLE-PLHENIDDDVLVIPENEYCOSEHMTIFVSIITAYKGLLVFGAF 639

QY 663 LAYETRSIKVKQINDSRVCMYNNVVVLLCLITAPVCMVIASQODASFAFVALVIFCCF 722

DB 640 LAWETRHVSIPALNDSKHGFSVYNVFTITLAGAAISLVLSDRKDLVLLSFIIFCTT 699

QY 723 LSMLLIFVPKIVBIRHPKDKAESKNP-----DSAIKSEDEERYQKLVTENEQ 771

DB 700 ATLCIVFVKLVKLNKPNQGVVKRVKVRATLRPMKNGRRDSSVC-ELEQRLRDVKNTNCR 758

QY 772 LQRLITQKEEKIRVLRQLRVERGDAKGTGLNGATGVASAAVATTSQP 818

DB 759 FRKALMEKENELQALIRKL---GPEARKWIDGVTCTGGSNVSGSELEP 802

RESULT 6

Q9VPS7 ID Q9VPS7 PRELIMINARY; PRT; 1305 AA.

AC Q9VPS7;

DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE CG3022 PROTEIN.  
 GN GABA-B-R3 OR CG3022.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY.  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang O., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Brill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Miklos G.L.G.,  
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Baldwin D.,  
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.B., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman J.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Munkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy L., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Scapleton M., Strong R., Sun E.,  
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003588; AAF51465.2;  
 DR FlyBase: FBgn031275; GABA-B-R3  
 DR InterPro: IPR001828; ANF\_receptor.  
 DR InterPro: IPR000337; GPCR\_Mgr.  
 DR Pfam: PF00003; 7tm\_3; 1.  
 DR Pfam: PF01094; ANF\_receptor; 1.  
 DR PRINTS: PR00248; GPCRMR.  
 DR PROSITE: PS50259; G\_PROTEIN\_RECEP\_F3\_4; 1.  
 DR PROSITE: PS00041; HTH\_ARAC\_FAMILY\_1; UNKNOWN\_1.  
 SQ SEQUENCE 1305 AA; 143588 MW; A9C3C85307650450 CRC64;

Query Match 23.4%; Score 1022.5; DB 5; Length 1305;

Best Local Similarity 29.1%; Pred. No. 4.7e-71;  
Matches 250; Conservative 171; Mismatches 348; Indels 91; Gaps 22;

QY 41 GIFPIA-GRGGWGGGACMPATRLALDDVNNKPNLLPGFKLILHSNDSECEPGIGASVMY 99  
 DB 157 GLFEUSTRGPRDGLSELGAATMAVEHINRK-RLPGYTLLELVNTDQCDPGVGVDRFF 215

QY 100 NLLYNKPKMLML--AGCSTVCTTVAEAAKMMNLIVLCYGASSPALSDDRRKPTPLRPTH 156  
 DB 216 HAITQSTRVAMLLGSACSEVETSLAKVYWNIVQVSGFSTPALSDDREFFYFTV 275  
 QY 157 PSATVHNPTRIKMKFGWSRVAILQAAEEVFISTVEDLENRCMEAGVEIYTRQSF-LSD 215  
 DB 276 APDSSHNPARIAFIRKFGWGVTTFSSQNEEVHSLAVNKLVTLEAANISCAATITFAATD 335  
 QY 216 PTDVARNLRRODARIIVGLFVVAARRVCEMYKOOLYGRAHVWF-----IGWEDNMY 270  
 DB 336 FKEQLLLRETDTRIIIGSGFQELAPQILCEAYRLRMFGADYAWILHESMGAPWPD--- 392  
 QY 271 EVNLKAEGITCTVEQMRIAARGHLTTAALMNNQNTTISGMTAEERHRLNOALIE-- 327  
 DB 393 -----QRTACSNHELQAVENLIVVSTHNSIVGNVNNYSISLNHMFNSQKQSAQPHG 446  
 QY 328 -----EGY-----DINHDR-----YPEGY-QEAPLAYDAVMSVALAF 358  
 DB 447 QDGFSGYGSRISTAATQSDSRRRRRGVGTSGGHLFPEALSQYAPQTYDAVMAIALAL 506  
 QY 359 NKTWE--RLFTGKSLRDFTYTDKEIADEIYAANNSTOFLGSGVGVAFSSOGDRIALFQI 416  
 DB 507 RAAEEHWRNRNEQSKLGDFTYTRSDMAWEFLQOMGKHLFLGSGVPVSFSGP-DRVGTTF 565  
 QY 417 EQMIDGKYEKLGYYDTQDNLNLSW----LNTQEWIGGKVPQDRTIVTHVLTVSLFLFCM 472  
 DB 566 YQIQGLLEPEVALYPADALDFRCPRCPRVKHSQGVPIAKRVKLRVATIAPLAFYTI 625  
 QY 473 CTISSCGIFVAFALIFINMKNHRRVIOSSHPVCNTIMLFVGIICLIIVLLGIDGREFV- 531  
 DB 626 ATLSVGLAIAEFLAFNLHFKLKAIKLSFKLSNTAVGCIFFVATVILLGLDHSILP 685  
 QY 532 -SPEEYPRKICQARAWLSTGTTLAYGAMFSKVRVHR-FTTKAKTDPKKKVPEPKLYTMV 589  
 DB 686 SAEDSFATVCTARVYLLSAGSLAFSGMSFAKTYRVHRIFTRTGSVFKDKMLQDIOLILV 745  
 QY 590 SGLSIDVLVLLSQIDPLQRYLETFFLEDPVSTTD-DIKIRPELEHCESSQNSMGLG 648  
 DB 746 GGLLVALLDVLVTVVTPDPMERHLNLTLE--ISATDRSVVYVQVQVCRSOHTQTLWSV 803  
 QY 649 VYGFGLLILFGLFLAYETRSIKVKQINDSRVGSNIYVNVVLCITAPVGVNVIASQDA 708  
 DB 804 LYAKGLLVGVVYMAWTRHVKIPALNDSQYIGVSVSVVITSIVVVLNLSISERVTL 863  
 QY 709 SFAFVALAVIPCCFLSMILLIFVPK-----VIEVIRHPKDKAESKYNPDSAISKEDE 759  
 DB 864 AFITITALLRTATATCCLLPKLHDIDPVIHSMG-LKMECNTRRFVYVDDRR 922  
 QY 760 ERYQKLVTEQLQRLITQKEEKIRVLRQLRVERGDAGKTELGATGVASAAVATTSQPA 819  
 DB 923 ELQYRVEVQNRVYKKEIQALDAEIRKL-ERLESG-----LTTTSTTTSSST 968  
 QY 820 SLINSSAHATPAATLAIITOG 839  
 DB 969 SLITGGGHLKP--ELTVTSG 986

RESULT 7

Q9BML5  
 ID Q9BML5 PRELIMINARY; PRT; 1305 AA.  
 AC Q9BML5;  
 DT 01-JUN-2001 (TReMBLrel. 17, Created)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE PUTATIVE METABOTROPIC GABA-B RECEPTOR SUBTYPE 3.  
 GN GABA-B-R3.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.

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RX PubMed=11168554;
RA Mezler M., Muller T., Raming K.;
RT "Cloning and functional expression of GABA-B receptors from
RT Drosophila.";
RL Eur. J. Neurosci. 13:477-486(2001).
KW EMBL; AF318274; AAK13422.1; -.
SQ SEQUENCE 1305 AA; 143701 MW; 8BBFA80F0E9BEADD CRC64;

Query Match 23.3%; Score 1018.5; DB 5; Length 1305;
Best Local Similarity 29.0%; Pred. No. 9.7e-71;
Matches 249; Conservative 171; Mismatches 349; Indels 91; Gaps 22;

QY 41 GIFFIA-GKGWGGQACMPATRLALDDVKNQPNLLPGFKLILHNSDSECEPLGLGASVMY 99
Db 157 GLFELSTSRGPRPDGLSELGAATMAVEHINRK-RLLPGYTLELVTNDTCQDGVGVDRFF 215
QY 100 NLLYNKQKMLL---AGCSTVCTTVAABAAMWNLIVLCYGASSPALSDRRKRPFLFRTH 156
Db 216 HAIYTOPSTRVMVLGSCASEVTESLAKVVPYWNIVQVSFGSTSPALSDRRREFFYRTV 275
QY 157 PSATVHPNTRIKLKKFGWSVAIIQQAEVFISTVEDLENRCMEAGVEIVTRQSF-LSD 215
Db 276 APDSHNPARTAFIRKFGWGTVFTFSQNEEVHSLAVNNLVTELEAANISCAATITFAATD 335
QY 216 PTDVARNLRQDARIIVGLFVVAARRVLCEMYKOQLYGRAHVWPF-----IGWEDNMY 270
Db 336 FKEQLLLLRDTRIIIGSFQELAPQILCEAYRLMEFGADYAWILHESMGAPWPD--- 392
QY 271 EVNLKAGITCTVCPRTAAEGHITTEALMNQNNQTTISGMTAEFRHLNQALIE--- 327
Db 393 -----QRTACSNHELQLAVENTLIVVSTHNSIVGNVSYSLNNHMFNSQLRKQSAQPHG 446
QY 328 -----EGY-----DINHNR-----YPEGY-QEAPLAYDAVWSVALAF 358
Db 447 ODGFGSGYGPRIATAQSDSRRRRGGVGTSGHGFPEPAISQYAPQYDAVWAIALAL 506
QY 359 NKTWE--RLATGKSLRDFTYTDEIAEIYAAMNSTQFLGVGGVAFSSQGDRIALQI 416
Db 507 RAAEHRWRNEEQKLDGFDYTRSDMAWEFLQMGKHLFLGVSGVPVSGP-DRVGTAF 565
QY 417 EQMIDGKYELGYYDTQDNLISW---LNTQEWIGGKVPQDRTIVTHVLRVSLPLFCM 472
Db 566 YIQRLLEPVALYYPATDALDFRCPRCPVKWHSQVPIAKRVFKLRVATIAPLAFYTI 625
QY 473 CTISSCGIFAVFALLIINWKNHRRVQSSHPVNTIMLFGVIICLSIVLLIGDGRV- 531
Db 626 ATLSVGIALAITFLAFNLHFRKLKAIKLSPPKLSNITAVGCIFFYATVILLGLDHSHP 685
QY 532 -SPEEYPKICQARAWLLSTGFTLAYGAMFSKVMRVHR-FTTKAKTDPPKKVPEPWKLYTMV 589
Db 686 SAEDSFATVCTARVYLLSAGSFLAGSMFATYRHRIFRTGTVKDKMLQDIOILILV 745
QY 590 SGLSIDVLWLSQIFDPLQRYLETFPLEDPVSTTD-DIKIRPELEHCSQSNMSWLGL 648
Db 746 GGLLVALLVTLWVVDPMERHLNLTLE--ISATDRSVYVQVQVEVCRSQHTQWLVS 803
QY 649 YVGFGLLIVFGLFLAVETRISIKVKQINDSRVGMISYNNVVLCLITAPGVGMVIAQODA 708
Db 804 LYAYKGLLVGVYMAWETRHVKIPALNDSQYIGVSVSVITSAIVVVLNLANLISERVTL 863
QY 709 SFAPVALAVFCCFLSMILLFVPR-----VIEVIRHPDKAESKYNPDSALSKEDE 759
Db 864 AFITAILITSTTATCLLFIPLKHLDIWARNDIIDPVHSMG-IKMECNTRRFVVDRR 922
QY 760 ERYQKLVTEBQRLITQKEEKIRVLQRQRLVERGDAKGTENGATGVASAAVATTSQPA 819
Db 923 ELQYRVEQNRVYKKEQALDAERKL-ERLLESG-----LTTTSTTSSST 968
QY 820 SLINSSAHATPAAPLAITQG 839
Db 969 SLLTGGGHLKP--ELTVTSG 986
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RESULT 8
ID Q23442 PRELIMINARY; PRT; 402 AA.
AC Q23442;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE COSMID ZK180.
GN ZK180.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roope A., Saunders D., Shownkeen R.,
RA Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Pauley A., Le T.T.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U58748; AAB52965.1; -.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR001064; Crystallin.
DR Pfam; PF00003; 7tm3; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
SQ SEQUENCE 402 AA; 45577 MW; D48DF0916CB4EFEE CRC64;

Query Match 10.4%; Score 457; DB 5; Length 402;
Best Local Similarity 29.9%; Pred. No. 1.7e-27;
Matches 132; Conservative 74; Mismatches 161; Indels 74; Gaps 15;

QY 389 ANNSTQFLGVGGVAFSSQGDRIALQIEQMIDGKYELGYDTQDNLISWLN--TEOWI 446
Db 15 AIDNSFQGLTGKVFAN-NERGLVDIKOWSDGQVTPFVAVYGDADDEKIIDSTTKGW- 72
QY 447 GGVVPQDRTIVTHVLTSLPLFVCMCTISSCGIFAVFALLIINWKNHRRVVIQSSHPVC 506
Db 73 --SPPLDSTITERRREHISILFLAM-----SLF-----IKMSSPNL 107
QY 507 NTIMLFGVITCLISVLLIGDRFVSPEYPKICQARAWLLSTGFTLAYGAMFSKVMRVH 566
Db 108 NNIIAGSICTEASVIMGLDTRIVSPDVFWLVCYTKTWTLCIGFTLSFGAMFSKTRVH 167
QY 567 RETTAKTDPKKVPEPWKLYTMVSGLLSIDLVILLSQIFDPLQRYLETFPLEDPVSTTD 626
Db 168 SIFTNIRMD-RAIKDSKLFILIGILLFIDICVLVTFWAFVSPFS-YTVT---ELPHIPED 222
QY 627 DIKIRPELEHCSQSNMSWLGLVYGFGLFLAVETRISIKVKQINDSRVGMISY 686
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Db 223 NTVLPEVEKCNSSHSQVFAVLAVKGVLMILGCLAWETHRVNVNVPALNDSKYIGTR-- 280  
Qy 687 NVVVLCLITAPVGMVIAQQDASFAFVALAVIFCCFL-----SMLLIFVPKVIEWIRHPDK 743  
Db 281 -----TGDRQVSREV-----FCHFLDNTNVVSREPCARDSKFKTPNFI 319  
Qy 744 AESKYNPDASISKEDE---ERYOKLVTENEQORLITQKEKIRVLQRILVERGDAGKTE 800  
Db 320 MKLFFN-----FSKNSYGFKNFKLSFGGFNVFARSQVKKVIELARNPV-----GNE 369  
Qy 801 LNG-ATGVASAAVATTSQPAS 820  
Db 370 PRAYRGLMKSVKATTSQPM 390  
PRT; 976 AA.  
RESULT 9  
Q9V485 PRELIMINARY; PRT; 976 AA.  
AC Q9V485;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE GLU-RA PROTEIN.  
GN GLU-RA OR CG11144.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Randell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
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RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
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RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveril J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195(2000).  
DR EMBL; AE003846; AAF59402.1; -.  
DR FlyBase; FBgn001985; Glu-RA.

DR InterPro; IPR001828; ANF\_receptor.  
DR InterPro; IPR000337; GPCR\_Mgr.  
DR Pfam; PF00003; 7tm3; 1.  
DR Pfam; PF01094; ANF\_receptor; 1.  
DR PRINTS; PR00248; GPCRMR.  
DR PROSITE; PS00979; G\_PROTEIN\_RECP\_F3\_1; 1.  
DR PROSITE; PS00980; G\_PROTEIN\_RECP\_F3\_2; 1.  
DR PROSITE; PS00981; G\_PROTEIN\_RECP\_F3\_3; 1.  
DR PROSITE; PS0259; G\_PROTEIN\_RECP\_F3\_4; 1.  
SQ SEQUENCE 976 AA; 108485 MW; 43A0ELF918EDACC4 CRC64;  
Query Match 8.3%; Score 362.5; DB 5; Length 976;  
Best Local Similarity 19.6%; Pred. No. 1.8e-19;  
Matches 202; Conservative 164; Mismatches 384; Indels 281; Gaps 40;  
QY 3 KDMTSDGAVTFWIFLCL-----IASP---HLQGVVA-GRPELHIGGIFPIACKGQWG 53  
DB 2 KQNNNGTILVVMVLSWSRVVDLKSPSNHTQDSVSVSLPGDILGLFPVHEKG---E 58  
QY 54 GQACMP-----ATRLALDDVKNQPNLLPGFKLILHSNDS----- 87  
DB 59 GAPCGPKVYNRGVQRLAEMLYAIDRVNNDPNILPGITIGVHILDTCSRDTVALNQSLOFV 118  
QY 88 -----ECEPGLGASVMTNLLYNKPKMLLAGCSTVCTVVAEAAKMNLLIVLC 135  
DB 119 RASLNNLDTSYECADGSSPQLRKN-ASSGPVFGVIGSSVSLQVANLLRLFLHFIQVS 177  
QY 136 YGASSPALSDRKRPPTLFRTHPSATVHNPTRIKLMKFGWSRVAILQQAEEVFISTVEDL 195  
DB 178 PASAKTLSDKTRFDLFARTVPPDTFQSVVALVDILKNFNWSYVTHISESGYGEYGEAL 237  
QY 196 ENRCMEAGVEIVTRQSFSLSDPTDAV-----RNLRRDARIIVGLVYVVAARRVLCCEMYK 249  
DB 238 HKEATERNVCIKAEKVPKADKVEDSILSKLQKKNARGVWLFTRAEDARRIL----- 292  
QY 250 QQLYGRAHVFFIGWY-EDNNYEVNKAEGI-----TCTVE-QMRIAAE-----GHULT 296  
DB 293 -QAAKRALNSQPFHIAISDGGKQKLEGLIEDIAEGAITVELQSEIITADFDYMMQLTP 351  
QY 297 E-----ALMW-----NONNOTTISGMTAEERHRLNQALI 326  
DB 352 ETNRNPFWEYEDTNCVLTSLVSPDTSNSANDTNKIGVRAKTKCDDSYRUSEKV- 410  
QY 327 EEGYDINHDPYEGYQEAFLAY--DAVMSVALAF-----NKTMERLTITCKSLRDT 376  
DB 411 --GYE-----QESKTFQVVDVAVAFAYALHNLHNDRCNTQSDQTTETRRHLSQES 458  
QY 377 YDKIEADEIYAA-----MNSTQFLGVSG-VVAFSSQGDRIALTQI-- 416  
DB 459 VVYRKISTDTKSOACPDAMANYDGRKEFYNNYLLNVSFIDLAGSEKVFDRQGDGLARYDILN 518  
QY 417 ----EQMIDGKYELGYDDTOLDNLNLSWLTNTQWIGKGPQDRTIVTHVLRVSLPLFCVM 472  
DB 519 YQROENSSGYQYKVGKWFNGLQ-----LNSETVVMNKETEQT-----SACSUPCEVGM 568  
QY 473 -----C-----TSSCG-----IF 481  
DB 569 IKKQGGDTCCWICDSCSEFEYVDEFTCKCGPGLVPYADKLSVALDIQYMKWNSLFL 628  
QY 482 VAFALIIFNI-----WNKHRRVYIQSSHPVCNTIMLVGVIICILISVILGIDGRF 530  
DB 629 IPMAIATFGIALTISIVILFAKNHDTPLVRASGRELSYTLFLGLVCYCNFTAL----- 682  
QY 531 VSPPEYFKI--QCARALLSTGFTFLAYGAMFSKVRVVR-FTTRAKTDPK-KKPEPWKLY 586  
DB 683 ---IAKPTIGSCVLQRFQIGVGFISIYSGALLTKNRISRFHSASAKSARLKYISPSQV 739  
QY 587 TMVSGLLSIDVALLSQIFDPLQRYLETFPLEDPVSTDDDKIRPELHESCESRNSMWL 646  
DB 740 VITSLIAIQLVLTIMWVVEP-----PGTRFYYPDRREVILKCKIQDMSEFLF 787  
QY 647 GLVYFGKGLILVFLGLAYETRSIKVKQINDSRVGMISYNNVWLCLITAPVGMVIAQQ 706

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Db 788 SOLNM--ILITICTIYAIAKTRKP-ENFNESKFIGFTMYTTCIIWLAFVPIYFTGNSY 844
QY 707 DASFAVALAIFCCFLSMILLIFVPKVIKIRHPRKDKAESKYNPDSAISKEDERYQKLV 766
Db 845 EVQTTICISISLSASVALCVLSPKVVILFHP-DKNVKLTMTNSTYRRAAQAQA 903
QY 767 TENQOLRLITQKEEKIRVLRQRLVERGDAKTE-LNG---ATGVASAAVATPSQ- 818
Db 904 PTSSGYSRT-----HAPCTSALTGGAVGTNASSSTLPTONSPHLDE 944
QY 819 ASLINSNAHAT 829
Db 945 ASQTNVAHKT 955

RESULT 10
Q62916
AC Q62916;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 4B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Hara P.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U47331; AAA86788.1; -.
DR InterPro: IPR000337; GPCR_Mgr.
DR InterPro: IPR001828; ANF_receptor.
DR Pfam: PF00003; 7tm_3; 1.
DR PRINTS: PR00248; GPCR_MGR.
DR PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE: PS0259; G_PROTEIN_RECEP_F3_4; 1.
SQ SEQUENCE 983 AA; 109276 MW; 072F0D8B3A840A80 CRC64;

Query Match 7.98; Score 343.5; DB 11; Length 983;
Best Local Similarity 19.0%; Pred. No. 5.6e-18;
Matches 170; Conservative 160; Mismatches 357; Indels 209; Gaps 35;
QY 5 MTSQGVTFW--IFLLCLIAS-----PHLOGGVAGRP-----DELHIGGIEPIAGK 48
Db 1 MSGKGGWAWMARLPLCLLLSLYAPWSPSSLGKPKGHPHMNSIRIDGDTLGLGFPVHGR 60
QY 49 GWMGGQAC-----MPATRLALDDVNKPNLLPGFKL----- 80
Db 61 G--SEGRACGLKKEKGHRLLEAMLFALDRINNDPDLPLNITLGARILDTCSRTHALEQ 118
QY 81 -----ILHNSDECEPGLGASVWYLLNYPKOKMLLAGC--STVCTTVAEAKMNNL 131
Db 119 SLTFVRLALIEKDGTEVRGSGGPP-----ITKPERVVGIVGASGSSVIMVANILRLFKI 174
QY 132 IVLCYGASSPALSRRKPTPLFRHPSPATVINPTRLKMKFGWSRVAIL-----QQA 184
Db 175 PQISYASTAPDLSNSRYDFSFVVPVSDTYQAQAVDITALKWNYVSTLASEGSYSGSG 234
QY 185 EEVFISTVDELENRCMEAGVIVTRQSFSLSDPTDAVRLRRQDARIIVGLEFVVAARVL 244
Db 235 VEAFIQSRNGGVGVCIAQSVKIPREPKTGEDPKIILKLETNSNARGIIFANEDDIRVL 294
QY 245 CEMYKOOLYGRAHWFFITGMYEDNW-----YEVNLKAEG-ITCTVQPMRIAEGHLLT 296
Db 295 EAARRANQTGH---FFWMG--SDSWGSKSAPVLRLEEVAEGAVTILPKRMSVRGDFRYS 349
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QY 297 EALMWNQNTTISGMTAEFEHRHLNQALIEGYDI-----NHDRYPB--GYQE---APLA 347
Db 350 SRTLDNRRNRNIWPAEFWEDNFKLKSRLHKGSHIKCTNRERIGQDSAEKGQVQFV 409
QY 348 YDAVWSVALAFNKTMRLTATGKKSRLDFTYTKDEIADEIYAAMNSTQFLGVSG-VVAFSS 406
Db 410 IDAVYANGHALHAMHRDLCPGRVGL--CPRMDPVDGTQLLKYIRNVNFSGIAGNPVTFNE 467
QY 407 QGDRIALTQTEQIMDGKYEKLYGYDQLDN-----LSW-----LNTQEWIGKVP 451
Db 468 NGD-----APGRYD---IYQQLRNGSAEYKVGISWTQDHLHLRIERMQWPGSGQQ 514
QY 452 QDRITVT-----HVLRT----- 463
Db 515 LPRISCSLPCQGERKTKVKGMACCNHCEPCTGYQYQVDRYTCCTPYDMRPTENRTSCQ 574
QY 464 -----VSLPLFVCMCTISSCGIFVAFALIIFINWKNHRRVIOSSHPCVNTIM 510
Db 575 PIPVVKLEWDSWAVLPLFLAVVGIAT-LFVVVTVFRYN-----DTPIVKASGRELSYVL 629
QY 511 LFGVIICLSVILLGIDGRFVSPPEYKPKICOARAWLLSTGFTLAYGAMFSKVVRVHRETT 570
Db 630 LAGIFLCYATTFLLM-----IAEPD--LGTCSLRRIFLGLGMSISYAALLTKTNRIYRFE 682
QY 571 KAK--TDPKKKVPKLYTMVSGLLSIDLVLLSWQIFDPLQRYLETFFPLEDPVSTDDI 628
Db 683 QGKRSYSAPRFTSPASQLAITFILISQLLGLICVWFVWDFSHSVVD---FQD--QRTLDP 737
QY 629 KIRPELEHESQNSMWGLVYFGKGLILVFLGFLAYETRSIKVKQINDSRYYGMSIYNV 688
Db 738 RFARGVLKCDI--SDLSLCLLGYSMMLMVTCTVYAKTRGV-ETFNKAPKIGFTMYTT 794
QY 689 VVLCILITAPVGMVIAQQDASFAFV-----ALAVIFCCFLSMLLIIVPKVIEVIRH 739
Db 795 CIVWLAFIPI--PFGTQSADKLIQTTLTIVSVLSASVSGLMYPKVIILFH 848

RESULT 11
Q6QYS2
ID Q6QYS2 PRELIMINARY; PRT; 879 AA.
AC Q6QYS2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 3 PROTEIN.
GN GRM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=20012997; PubMed=10544282;
RA Minoshima T., Nakanishi S.;
RT "Structural organization of the mouse metabotropic glutamate receptor subtype 3 and its regulation by growth factors in cultured cortical astrocytes.";
RL J. Biochem. 126:889-896(1999).
DR EMBL: AF170701; AAF06741.1; -.
DR EMBL: AF170697; AAF06741.1; JOINED.
DR EMBL: AF170698; AAF06741.1; JOINED.
DR EMBL: AF170699; AAF06741.1; JOINED.
DR EMBL: AF170700; AAF06741.1; JOINED.
DR InterPro: IPR00337; GPCR_Mgr.
DR InterPro: IPR001828; ANF_receptor.
DR Pfam: PF00003; 7tm_3; 1.
DR Pfam: PF01094; ANF_receptor; 1.
DR PRINTS: PR00248; GPCR_MGR.
DR PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE: PS0259; G_PROTEIN_RECEP_F3_4; 1.
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Db 204 PFSRVVPPDSYQAQAVDIVKALGNVYFILASEGNYGESVDADFVQISREAGGLCIAQS 263  
QY 204 VEIVTRQSLSDPT-----DAV--RNLRDARIIIVGLVYVAARRVCEMYKQOOLYGRAH 257  
Db 264 MKIP-----RDPKGEFDKIIKRLMETPNARGIIIFANEDDITKQVLEAARRANLTCG-- 315  
QY 258 VWFELGWEDNW-----YEVNLKAGGITCTVQEMRIAAEG---HLTTEALMWNQN 304  
Db 316 -FKFVG--SDSGAKSAPILDNEEV---AEG-AVTILPKRASVEGDFQYFTSRSL---EN 365  
QY 305 NQTTI--SGMTAEFHRNLQALIE-----EGYD-INHDKRYPEGYQCAPLAYDAVWS 353  
Db 366 NERNIWAEEFEDDECKLIRGKILDPKKCTGERIGRDSPEYQEGKVQVIVADAYA 425  
QY 354 VALAFNKMTMERLTTGKKSLRDTYTDKEIADEIYAAMNSTQFVLGSGV-VAFSSQGDRIA 412  
Db 426 MAHALHNMHOTCARGRTLCKMDPVEGRLLLSYIRAVN---FNGSAGTGVLFENEGD--- 479  
QY 413 LQIEOMIDGKYEKLYGYDTQDNLNLS-----WLTNT--- 442  
Db 480 -----APGRYDIFQY---QFSNTSPGYKVIGQSFSISSAKTSSPGYKVFQOWTNLGG 529  
QY 443 -----EQWIGGK----- 449  
Db 530 INEVEEMQSGGEHYIPASVCFPCOPGERKKMVKGVPCCHCEPCDGYQYQVGEELTCM 589  
QY 450 VPQD-RTIVTHVLRVTS-----LPLFVCMCTISSGIFVAFALIIFNIWNKH 495  
Db 590 CFPDMRPTANHTACTPTPIIKLDHSPWAVVPMFLAI-----LGIATLSVIVFVREND 644  
QY 496 RRVIOSSHVPVNTIMLFGV-IICLISVILLGIDGRVSPBEYFKICQARAWLLSTGFTLA 554  
Db 645 TPIVASGRELVSVLGTGFLIYLITFLMTA-----EPNTVVCALRLLGLGMCIT 696  
QY 555 YGAMESKVMVRHFTTKAK---TDPKKVPEPKLYMTWSGLLSIDILVILLSWQIFDPLQR 611  
Db 697 YSAMLTKTRNRIYRIFQGGKSVTAP-KFISPTSQLVITFLVSEFQVIGVPIW----- 747  
QY 612 YLETPLEDVSTDDIKIR---PELEH---CESQNSMWGLVYGFKGLIILVFLGLFA 664  
Db 748 ----FGVPPHTIVDYDELRPNPPELARGILKCDMSDLSLICLSYSI--LLMVTCTVYA 801  
QY 665 YETRSKVKQINDSRVGMISYVNVVLCITAPV--GMVIASQODASFAPVALAVIFCCF 722  
Db 802 VKSRGVP-ETFEAKPIGFTMTTCTVWLAFVPIFFGTAQSHGEDV----- 846  
QY 723 LSWLLIFVPKVIIEVIRHPKDKAESKYNPD 751  
Db 847 -----HPDDHADRVHEPE 859  
  
RESULT 15  
Q98UC5  
ID Q98UC5 PRELIMINARY; PRT; 1188 AA.  
AC Q98UC5;  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE METABOTROPIC GLUTAMATE RECEPTOR 5 SPLICED VARIANT B.  
GN MGIUR5B.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RA \*Johann L.L., Stormann T.M., Parks T.N.;  
RT Molecular Cloning and Functional Expression of Chick Metabotropic  
RT Glutamate Receptor 5 Splice variants.\*;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF227202; AAK01487.1; .

KW Receptor. 1188 AA; 132053 MW; 6CL179BF8C8045BBD CRC64;  
SQ SEQUENCE  
  
Query Match 6.8%; Score 299.5; DB 13; Length 1188;  
Best Local Similarity 20.1%; Pred. No. 2.1e-14;  
Matches 202; Conservative 153; Mismatches 395; Indels 253; Gaps 40;  
  
QY 16 FLCLIASPHLQGVAGRPDELHIGGIFPI-----AGKGGWGGQACMPATR 62  
Db 20 FGLLVSAQANRRVVAHMPGDIIGALFVHHQPTVDKVERKCGVEQYGIQVRAEML 79  
QY 63 LALDDVKNQNLPLGFKLILHSND-----SECEPGL-----GA 95  
Db 80 HTLDRLNLTPLTNITLGEIRDSCWHSVALEQSTIEFRDLSLISEEEGVRCDVGS 139  
QY 96 SVMYNNLYNPKQKMLLAGCSTVCTTVAEAAKMMNLVLCYGASSPALSDDRKPFTLFT 155  
Db 140 SSSFH--SKPIVGVIGPGSSVAIQONLLQFNIPQIAYSATSMDSKTLFKYPMRV 197  
QY 156 HPSATVHNPTRIKLMKFGMSRVAILQQAEEVFISTVEDLENRCMEAGVEIVTRQSLSD 215  
Db 198 VPSDAQARAMVDIVKRYNNTYVSAVHTEGYSGMEAFKMAAKKEGICIAHSYKIYSN 257  
QY 216 PTD-----AVRNLRQ--DARIIVGLFYVAARRVLCMYKQOLYGRAHVVFFIGWEDN 268  
Db 258 AGEQSFDKLLRKLRLSHLPKARVAVACFCGEMTVRGLLMAMRLGLAGE-----FLLGSDG 312  
QY 269 WYEVNLKAEGITCIVEQMRIAAG---HLTTEALMWNQNTTISGMT-----AEEFR 318  
Db 313 W-----ADRYDVTGQREAVGGITIKLQSPDVKWFDYDYLELRPETNHRNPFQEFWQ 366  
QY 319 HRLNQALIEGYDINHRY-----PEGYQEAFLAY--DAVWSVALAFNKTMERL 365  
Db 367 HRFQRL--EGFPOENPKYKNTCTSQMTRTQHVQDSKMGFVINAIYSMAVGLHNMQLSL 424  
QY 366 TTGKKSRLDFTYDKEI-ADBIYAAMNSTQPLGVSG-VVAFSSQGDRIALQIEOMIDGK 423  
Db 425 CPGVVGLCD---AMKPIDGRKLLSLMKTNTFTVSGDMILFDENGDS-----PGR 471  
QY 424 YEKLYGYDTQDNLNLSWNTQEWIGGKVPQDRTIV---THVLRV-SIPL----- 468  
Db 472 YEIMNFKKMGKDYDYINVGSWDMGELKMDDEIWESEKNNIIRSVCEPCEKQIKVIRK 531  
QY 469 -----FVC-MCTISS-----CGIF-----VA 483  
Db 532 GEVSCWCTCPKENEYVEDEYCTKACQLGSPWDELGTCLIPQVLRWGDPEPIAAV 591  
QY 484 FALI-----IFNIWNKRRVIOSSHPVCMVIMLFGVII-----CLISVILLGID 527  
Db 592 FACIGLLATLFTVTAIFTMYRDTVPVKSRSRELC-YIILAGICLGYLCTFCLIA----- 643  
QY 528 GRFVSPEYKICQARAWLLSTGFTLAYGAMFSKVRVHRETTAKTDPKKKVPKWLKT 587  
Db 644 ----KPOOI---YCYLQIGIGLSPAMSYLSALVTNTRILAGS---KKKCTKPRF 693  
QY 588 MVSGLLSIDLIVLLSWQIFDPLQRYLETFLPEDPVSTDDIKIRPELHESQNSMWLG 647  
Db 694 MSACAQLVIAFILICIQ---LGIIVLALFIMEPDDIMHDYPSIREVYLIC---NTNIG 745  
QY 648 LV--YGFKGLILVFLGLFLAYETRSIKVKQINDSRVGMISYVNVVLCITAPVGMVIASQ 705  
Db 746 VVPLGYNGLLILSCTGFYAFKTRNVPA-NFNEAKYIAFTMTYTCIIWLAFVPI----- 797  
QY 706 QDASFAPVALAVIFCCF-----LSMLLIFFVPKVIEWIRHPKDKAESKYNPD 754  
Db 798 ----YFGSNYKIITWCFVSLSATVALGCMFVPKVYIILAKPERNVRSAFTTSTVVRMHV 853  
QY 755 ----SKEDERYQKLV-----TENEOL---ORLTQKEKIRVLRQRLVERGDAKGT 799  
Db 854 GDGKSSAAASRSSSLVNLWKRGGSGFTLYKGRRLAPHKSE-----IECTPKGS 904  
QY 800 ELNG--ATGVASAAVATTSSQASLINSASHATPAATLAIQGE 840

Db 905 MCGGRATMTSSNGKSYSWAQNEKSSRCAGHLWORLSIHINKKE 947

Search completed: April 30, 2002, 10:16:30  
Job time: 237 sec